GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

September 3, 2003, 11:25:42; Search time 9.25 Seconds
(without alignments)
101.679 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-087-464-1 104 1 GMPWLSATTVRSVTHANALT 20

127863 seqs, 47026705 residues Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	•	62 rattus norv				-	46 oryctolagus		_						_	v2 rattus norv	91 homo sapien	83 methanobact	56 rattus norv	73 mus musculu	_			80 mycobacteri		.04 schizosacch	10 escherichia	76 escherichia	34 rhodospiril	-	canl	85 sus scrofa
esc	P027	P23562	P15575	P32847	P23347	P13808	P48746	P04920	P16283	P23348	P48751	018917	092088	Q9gky1	329	Q8k4v2	096q91	027083	P51556	088673	008447	Q8nbs3	095708	010380	P00749	Q9c104	P32710	P14176	P23134	003603	09abz8	0418
Ω	ο.	ם הם	ι α,	щ	Д	Д,	Д	Δ,	Д	Δ,	Д	0	a	α	0	a	a	0	Δ,	0	0	a	ø	æ	Δ,	O.	Ω,	Д	щ	a	о	Ā
	B3AT_HUMAN	B3AT_RAT	B3AT_CHICK	B3AT_ONCMY	B3A2_RAT	B3A2_MOUSE	B3A2_RABIT	B3A2_HUMAN	B3A3_MOUSE	B3A3_RAT	B3A3_HUMAN	B3A3_RABIT	B3A2_CAVPO	B3A4_RABIT	LIPA_MYCLE	B3A4_RAT	B3A4_HUMAN	COBK_METTH	KDGA_RAT	KDGA_MOUSE	C13A_MYCTU	SL11_HUMAN	NU3M_HYLLA	LIPA_MYCTU	UROK_HUMAN	YKT5_SCHPO	NRFE_ECOLI	PROW_ECOLI	CYB_RHORU	KDGL_CAEEL	- 1	UROK_PIG
DB	-			Н		Н	7	-	~	Н	Н	-1	٦	Н		~	-	7	-	-										-		-
Length	911	927	922	918	1234	1237	1237	1241	1227	1227	1232	1233	1238	955	314	953	983	302	727	730	449	891	115	311	431	1076	552	354	405	827	322	442
% Query Match	100.0	100.0	96.2	91.3			4.68	•	85.6	85.6	85.6	85.6		47.1					٠		42.3		41.3	41.3	41.3	⊣	0	0	0	40.4	39.4	39.4
Score	104	104	100	95	93	93	93	93	88	83	83	88	83	49	48	48	48	45	45	45	44	44	43	43	43	4	42.5	42	42	42	41	41
Result No.	- H	(A) (L	→	'n	Q	7	œ	σ	10	11	12	13	14	12	16	17	18	19	20	21	22	23	24	25	26	27	28	53	30	31	32	33

P11078 reovirus (t	P20192 sus scrofa	P42703 mus musculu	P12915 b genome po	Q91z10 mus musculu	Q9nyq7 homo sapien	088278 rattus norv	Q64319 rattus norv	P51208 porphyra pu	P56938 rhodobacter	P07519 hordeum vul	P15321 serratia ma	
VM2_REOVD	KDGA_PIG	LIFR_MOUSE	POLG_BOVEV	CLR3_MOUSE	CLR3_HUMAN	CLR3_RAT	SC31_RAT	YC56_PORPU	COXX_RHOSH	CBP1_HORVU	HLYB_SERMA	
7	7	Ţ	Т	7	Т	Н	Н	Н	Н	-	Н	
709	734	1092	2175	3301	3312	3313	683	263	284	499	557	
39.4	39.4	39.4	39.4	39.4	39.4	39.4	38.9	38.5	38.5	38.5	38.5	
41	41	41	41	41	41	41	40.5	40	40	40	40	
34	35	36	37	38	38	40	41	42	43	44	45	

ALIGNMENTS

RY SCIONING and Characterization of band 3, the human erythrocyte anion archange protein (REI)."; RY Cloning and characterization of band 3, the human erythrocyte anion acchange protein (REI)."; RY EXCHANGE PROTEIN (REI)."; RY STOURNCE FROM N.A. RY Tanner M.J.A., Martin P.G., High S.; RY ELINE-90001204; Pubmed-3229043; RY SEQUENCE OF 1-199; 220-292 AND 347-370. RY MEDLINE-90001204; Pubmed-2790053; RY MEDLINE-90001204; Pubmed-2790053; RY Primary structure of the cytoplasmic domain of human erythrocyte membrane band 3. Comparison with its sequence in the mouse."; RY Primary structure of the cytoplasmic domain of human erythrocyte membrane band 3. Comparison with its sequence in the mouse."; RY MEDLINE-9023186; Pubmed-5345535; RA MEDLINE-9027186; Pubmed-701248; RY Manion acid Sequence of the N alpha-terminal 201 residues of human erythrocyte membrane band 3.", RY MEDLINE-79027186; Pubmed-701248; RY MEDLINE-79027186; Pubmed-701248; RY MEDLINE-79027186; Pubmed-701248; RY MEDLINE-7900186; Pubmed-701248; RY MEDLINE-70027186; Pubmed-70124	Part HUMAN STANDARD; PRT; 911 AA. 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Created) 15-SEP-2003 (Rel. 14, Last sequence update) 15-SEP-2003 (Rel. 14, Last annotation update) 16-CD23 antigen) 18-SEP-2003 (Rel. 14, Last annotation update) 18-DEP-2003 (Rel. 14) 18
--	--

```
ם.
                                                                                                                                                                                                                                                                                                                                                                                          "Sequential phosphorylation of protein band 3 by Syk and Lyn tyrosine kinases in intact human erythrocytes: identification of primary and secondary phosphorylation sites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-91329825; PubMed-1678289; Yannoukakos D., Vasseur C., Driancourt C., Blouquit Y., Delauney J., Wasseur B., Bursaux E., Brisaux E., "Human erythrocyte band 3 polymorphism (band 3 Memphis): characterization of the structural modification (Lys 56-->Glu) by protein chemistry methods."; Delood 78:1117-1120(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT HE 400-ALA--ALA-408 DEL, AND VARIANT MEMPHIS GLU-56.
MEDLINE-92107882; PubMed-1722314;
Jarolim P., Palek J., Amato D., Hassan K., Sapak P., Nurse G.T.,
Kubin H.L., Zhai S., Sahr K.E., Liu S.-C.;
"Deletion in erythrocyte band 3 gene in malaria-resistant Southeast
Asian ovalocytosis";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT HE 400-ALA--ALA-408 DEL.
MEDLINE-92167271; PubMed-1538405;
Schofield A.E., Tanner M.J.A., Pinder J.C., Clough B., Bayley P.M.,
Nash G.B., Dluzewski A.R., Reardon D.M., Cox T.M., Wilson R.J.M.,
conformation and a possible molecular mechanism for anion
                                                                                                                                                                                                                                                                                                                                              PHOSPHORYLATION OF TYR-8; TYR-21; TYR-359 AND TYR-904.
BEDLINE-20400020; Dubmed-10942405;
Brunati A.M., Bordin L., Clari G., James P., Quadroni M., Baritono i Pinna L.A., Donella-Deana A.;
                                                                                                                                                                                                                                                      Okubo K., Hamasaki N., Hara K., Kageura M.;
"Palmitoylation of cysteine 69 from the COOH terminal of band 3 protein in the human erythrocyte membrane. Acylation occurs in the middle of the consensus sequence of F--I-IICLAVI found in band 3 protein and G2 protein of Rift Valley fever virus.";
J. Biol. Chem. 266:16420-16424(1991).
                                              SEQUENCE OF 834-911.
MEDLINE-88228050; PubMed-3372523;
MEDLINE-88228050; PubMed-3372523;
Miyata T., Iwanaga S., Hamasaki "Localization of the pyridoxal phosphate binding site at the COOH-terminal region of erythrocyte band 3 protein.";
J. Biol. Chem. 263:8232-8238(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cohen C.M.;
Band 3 Tuscaloosa: Pro-327-->Arg substitution in the cytoplasmic
domain of erythrocyte band 3 protein associated with spherocytic
hemolytic anemia and partial deficiency of protein 4.2.";
Blood 80:523-529(1992).
                                                                                                                                                                               m
                                                                                                                                                                             human red blood cell band
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-92329950; PubMed-1378323;
Jarolim P., Palek J., Rubin H.L., Prchal J.T., Korsgren C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                properties in hereditary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 88:11022-11026(1991).
                                                                                                                                        ROLE OF GLU-681, AND SEQUENCE OF 665-688.
MEDLINE-92332495; PubMed-1352774;
                                                                                                                                                                Jennings M.L., Smith J.S.; Anion-proton cotransport through the
                                                                                                                                                                                          protein. Role of glutamate 681.";
J. Biol. Chem. 267:13964-13971(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gratzer W.B.;
"Basis of unique red cell membrane
                                                                                                                                                                                                                                          MEDLINE=91358422; PubMed=1885574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-93343855; PubMed-8343110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol. Biol. 223:949-958(1992)
                        31ochem. J. 213:577-586(1983).
                                                                                                                                                                                                                               PALMITOYLATION OF CYS-843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /ARIANT MEMPHIS GLU-56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT HS ARG-327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT HS LEU-868.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ovalocytosis
 sednence,
                exchange
                                                                                                                                                                                                                                                                                                                                  10]
```

```
VARIANTS HS GLN-760; TRP-760; CYS-808 AND TRP-870.
MEDLINE-95134993; PubMed=7530501;
Jarolin P., Rubin H.L., Brabec V., Chrobak L., Zolotarev A.S.,
Alper S.L., Brugnara C., Wichterle H., Palek J.;
"Mutations of conserved arginines in the membrane domain of erythroid band 3 lead to a decrease in membrane-associated band 3 and to the phenotype of hereditary spherocytosis.";
Blood 85:634-640(1995).
                                                                                                                                                                                                                                                                                                                                                                                                         "Human erythrocyte protein 4.2 deficiency associated with hemolytic anemia and a homozygous 40 glutamic acid-->lysine substitution in the cytoplasmic domain of band 3 (band 3Montefiore)."; Blood 81:2155-2165(1993)
Bruce L.J., Kay M.M., Lawrence C., Tanner M.J.;
"Band 3 HT, a human red-cell variant associated with acanthocytosis
and increased anion transport, carries the mutation Pro-868-->Leu in
the membrane domain of band 3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT BLOOD GROUP DI(A)/MEMPHIS-II.
MEDLINE-9456802; PubMed-8206915;
MEDLINE-9456802; PubMed-8206915;
BBUCCE L.J., Anstee D.J., Spring F.A., Tanner M.J.;
"Band 3 Memphis variant II. Altered stilbene disulfonate binding and the Disgo (Dia) blood group antigen are associated with the human errythrocyte band 3 mutation Pro-854-->Leu.";
J. Biol. Chem. 269:16155-16158(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bozon M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT HS ASP-771.
MEDLINE-96136073; PubMed-8547122;
Maillet P., Vallier A., Reinhart W.H., Wyss E.J., Ott P., Texier P.,
Baillet F., Tanner M.J., Delaunay J., Alloisio N.;
Baklouti F., Tanner M.J., Delaunay J., Alloisio N.;
"Band 3 Chur: a variant associated with band 3-deficient hereditary
spherocytosis and substitution in a highly conserved position of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tanner M.J.;
Changes in the blood group Wright antigens are associated with a
mutation at amino acid 658 in human erythrocyte band 3: a site of
interaction between band 3 and glycophorin A under certain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARÍANTS HS LYS-40; CYS-518 AND MET-663 DEL.
MEDLINE-9622450, Pubmed-8464029,
Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,
Dornwell M., Herbers J., Kugler W., Oezcan R., Pekrun A.,
Galladper P.G., Schroeter W., Forget B.G., Lux S.E.;
"Ankyrin-1 mutations are a major cause of dominant and recessive hereditary spherocytosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97351102; PubMed-9207478;
Alloisio N., Texier P., Vallier A., Ribeiro M.L., Morle L., Bozoi
Bursaux E., Maillet P., Goncalves P., Tanner M.J., Tamagnini G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Characterization of 13 novel band 3 gene defects in hereditary spherocytosis with band 3 deficiency."; Blood 88:4366-4374(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jarolim P., Murray J.L., Rubin H.L., Taylor W.M., Prchal J.T., Ballas S.K., Snyder L.M., Chrobak L., Melrose W.D., Brabec V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT BLOOD GROUP WR(A).
MEDLINE-95111140; PubMed-7812009;
Bruce L.J., Ring S.M., Anstee D.J., Reid M.E., Wilkinson S.,
                                                                                                                                                                                                                                                                                          MEDLINE-93229758; Pubmed-8471774;
Rybicki A.C., Qiu J.J.H., Musto S., Rosen N.L., Nagel R.L.,
Schwartz R.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANTS HS ASP-285; GLU-455; PRO-707; PRO-834 AND MET-837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transmembrane segment 11.".
Br. J. Haematol. 91:804-810(1995).
[21]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97099297; PubMed-8943874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANTS HS SER-147 AND MET-488
                                                                                                                                                                       Biochem. J. 293:317-320(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13:214-218(1996).
                                                                                                                                                                                                                                                       VARIANT MONTEFIORE LYS-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blood 85:541-547(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Palek
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KUGTYCKI K.E., Shull G.E.;
Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
-!- Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
-!- EUNCTION: BAND 3 HAS TWO FUNCTIONAL DOMAINS: ITS INTEGRAL DOMAIN EDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS THE MEMBRANE, WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING SITES FOR CYTOSKELETALA AND OTHER PROTEINS (BY SIMILARITY).
-!- SUBUNIT: A DIMEN IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY AND APPEARS TO BE TETRAMERIC.
-!- SUBMIT: A DIMEN LOCATION: INTEGRAL MEMBRANE PROTEIN. IN THE BASOLAFERAL MEMBRANE OF INTERCALATED CELLS OF DISTAL TUBULES AND COLLECTING DUCTS.
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota: Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kudrycki K.E., Shull G.E.; "Primary structure of the rat kidney band 3 anion exchange protein
                                                                                                                                                                                                                                                                                                                                                                                                                                       EB-2003 (Rel. 41, Last sequence update)
EB-2003 (Rel. 41, Last annotation update)
3 anion transport protein (Anion exchange protein 1) (AE 1).
                                                                   ö
Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00219; ANION EXCHANGER 1; 1.
PROSITE; PS00220; ANION EXCHANGER 2; 1.
Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;
                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY: Kidney.
SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
      ; DB 1;
4.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event-Alternative splicing; Named isoforms-2;
                                                                                                                                                                                                                                                                                                                                                927 AA.
                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Kidney;
IsoId=P23562-2; Sequence=VSP_000455;
100.0%; Score 104;
100.0%; Pred. No. 4
:ive 0; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId-P23562-1; Sequence-Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HGO3_cotranspt.
Pfam; PF00955; HGO3_cotranspt.
PRINTS; PR01231; HGO3TRNSPORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   deduced from a cDNA.";
J. Biol. Chem. 264:8185-8192(1989).
                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; J04793; AAA40800.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Kidney;
MEDLINE=89255254; Pubmed=2722777;
                                                                                                                                                           720 GMPWLSATTVRSVTHANALT 739
                                                                                                                              1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, L02943; AAA40801.1; -- PIR; A33810; A33810. HSSP; P02730; 1BTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 46-927 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-45 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGRFAMS; TIGR00834; ae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALTERNATIVE PRODUCTS:
                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name-Erythrocyte;
                                Local Similarity
nes 20; Conser
                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1991 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLC4A1 OR AE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003
   Query Match
                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Band
                                                                                                                                                                                                                                                                                                            | B3AI_RAT | B3AI_RAT | B3AI_RAT | B3AI_RAT | B3AI 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <del>-</del>-
                                                                                                                                                                                                                                                                                   RESULT 2
                                                                                                                                                                                        g
                                                                                                                              å
```

```
SEQUENCE FROM N.A.
MEDLINE-85268011; PubMed-2410791;
Kopito R.R., Lodish H.F.;
"Primary structure and transmembrane orientation of the murine anion
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                              PALMITATE (BY SIMILARITY).
Missing (in isoform Kidney).
/Frid=VSP_000455
                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                             13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Band 3 anion transport protein (Anion exchange protein 1). (AE
                                                                                                                                                                                                                                                                   Length 927;
                                                                                       EXOPLASMIC LOOP (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARTIAL SEQUENCE FROM N.A.
MEDLINE-87250387; PubMed-3036795;
Kopito R.R., Andersson M., Lodish H.F.;
"Structure and organization of the murine band 3 gene.";
J. Biol. Chem. 262:8035-8040(1987).
                                                                                                                                    EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUL-1987) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                            681A228474E5E9DE CRC64;
native splicing.
CYTOPLASMIC (POTENTIAL).
MEMBRANE (ANION EXCHANGE)
                                                                                                              CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-86634211; PubMed-3840489;
ROPITO R.R., Lodish H.F.;
"Structure of the murine anion exchange protein.";
J. Cell. Biochem. 29:1-17(1985).
                                                                                                                                                                                                                                                                  100.0%; Score 104; DB 1; 100.0%; Pred. No. 4.4e-09;
                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                          929 AA.
                                                                                                                                                                                                                                                                                         Mismatches
                                                        POTENTIAL.
                                                                   POTENTIAL.
                                                                                                                       POTENTIAL.
                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                        POTENTIAL.
                                   POTENTIAL
                                             POTENTIAL
                                                                              POTENTIAL
                                                                                                                                               POTENTIAL
                                                                                                                                                         POTENTIAL
  Alternative
                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                          736 GMPWLSATTVRSVTHANALT 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 11-929 FROM N.A.
MEDLINE-86274622; Pubmed-3015590;
                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                              927 AA; 103172 MW;
                                                                                                                                                                                                                                                                                                               1 GMPWLSATTVRSVTHANALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exchange protein.";
Nature 316:234-238(1985).
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
  Palmitate;
            420
927
441
473
496
527
528
585
604
619
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                 779
801
860
658
859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLC4A1 OR AE1
 Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                        B3AT_MOUSE
P04919;
                                                                                                                                                                                       TRANSMEM
CARBOHYD
                        DOMAIN
TRANSMEM
                                                                 TRANSMEM
                                                                                                                                                                                                                         VARSPLIC
                                                                                                                                                                                                                                              SEQUENCE
                                                                                                  FRANSMEM
                                                                                                                        FRANSMEM
                                                                                                                                              FRANSMEM
                                                                                                                                                                   LRANSMEM
                                                                                                                                                                               TRANSMEM
                                                                                                                                                         FRANSMEM
                                           TRANSMEN
                                                        PRANSMEN
                                                                                       DOMAIN
                                                                                                              DOMAIN
                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MEB3)
                                                                                                                                                                                                                                                                                                                                                                                B3AT_MOUSE
                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
  g
```

ö

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                   HEMOGLOBIN.
SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY
AND APPEARS TO BE TETRAMERIC.
SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                   ACROSS
                                                                                                                                                                           'Major proteolytic fragments of the murine band 3 protein as obtained
                                                                                                                         MEDLINE-89229233; PubMed-2713407;
Raida M., Wendel J., Kojro E., Fahrenholz F., Fasold H., Legrum B.,
                                                                                                                                                                                                                           -1- FUNCTION: BAND 3 IS THE MAJOR INTEGRAL GLYCOPROTEIN OF THE ERYPHROCYTE MEMBRANE. BAND 3 HAS TWO FUNCTIONAL DOMAINS. ITS INTEGRAL DOMAIN MEDIATES A 1:1 EXCHANGE OF INDEGRAL AND AT THE MEMBRANE, WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING SITES FOR CYTOSKELETAL PROTEINS, GLYCOLYTIC ENZYMES, AND
                  Cloe L., Rovera G., Curtis P.J.; "Cloning and structural characterization of a human non-erythroid
Demuth D.R., Showe L.C., Ballantine M., Palumbo A., Fraser P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X02677; CAAA5506.1; -
REBL; M29379; AAA37187.1; -
REBL; M29379; AAA37555.1; -
REBL; X03917; CAAA7555.1; -
REPL; REBL; X03919; X0.41
REPL; REPL; RERO03177; Anion_exchange.
REPL; REPL; RERO0325; HCO3_cotranspt.
REPL; REROS123; HCO3_cotranspt.
REPL; RERO0325; HCO3_cotranspt.
REPL; RERO0325; HCO3_cotranspt.
REPROSITE; PS00219; ANION_EXCHANGER_1; 1.
REPROSITE; PS00219; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL. EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISOId=P04919-2; Sequence-VSP_000454;
TISSUE SPECIFICITY: ERYTHROCYTE.
SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lipoprotein; Palmitate; Alternative splicing.

1 422 CYTOPLASMIC (POTENTIAL).

DOMAIN 423 929 MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                        Event-Alternative splicing; Named isoforms=2;
                                                                                                         SEQUENCE OF 33-47; 360-375; 382-395 AND 578-590.
                                                                                                                                                                                                                                                                                                                                                                                                                         Name=Erythrocyte;
IsoId=P04919-1; Sequence=Displayed;
                                                                                                                                                                                               after in situ proteolysis.";
Biochim. Biophys. Acta 980:291-298(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                     band 3-<u>ľike protein.";</u>
EMBO J. 5:1205-1214(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4443
475
475
529
560
606
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name-Kidney
                                                                                                                                                              Passow H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- SUBUNT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY AND APPEARS TO BE TETRAMERIC.
-i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- TISSUE SPECIFICITY: BRYTHROCYTE.
-i- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE-89039870; PubMed-3185555;

Kim H.R.C., Tew N.S., Ansorge W.D.

Kim H.R.C., Tew N.S., Ansorge W.D.

Wennstroem B., Zenke M., Engel J.D.;

"Two different mRNAs are transcribed from a single genomic locus encoding the chicken errythrocyte anion transport proteins (band 3).";

Mol. Cell. Biol. 8:4416-4424(1988).

I-FUNCTION: BAND 3 IS THE MAJOR INTEGRAL GLYCOPROTEIN OF THE ERYTHROCYTE MEMBRANE. BAND 3 HAS TWO FUNCTIONAL DOMAINS. ITS INTEGRAL DOMAIN MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS INTES FOR CYTOSKELETAL PROTEINS, GLYCOLYTIC ENZYMES, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .01-APR-1990 (Rel. 14, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Band 3 anion transport protein.
Gallus gallus (Chicken).
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                         ;
0
                                                                                                                                                                Length 929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Missing (in isoform Kidney).
/FIIda-VSD-000454.
G -> S (IN REF 5).
V; 5C0E281C394FB614 CRC64;
                                                                                                                                                                                                                         Indels
     PALMITATE (BY SIMILARITY).
                                                                                                                                                                Score 104; DB 1;
Pred. No. 4.4e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       922 AA.
                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotranspt.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                            UNITION OF TAXABLE TO STATE TO
                                                                                                                                                                                                                                                                                1 GMPWLSATTVRSVTHANALT 20
                                                                                                               103135 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1990 (Rel. 14, Created)
                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M23404; AAA48753.1; -. HSSP; P02730; 1BTQ.
                                                                                                                                                                                                  100.08;
                                                                                                                                                                   Query Match 100.0
Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
861
79
                                                                                     467
                                                                                                               929 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9031;
  861
                                                                                     467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEMOGLOBIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B3AT_CHICK
P15575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
TRANSMEM
                                                                                                                  SEQUENCE
                            VARSPLIC
                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
B3AT_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FT
                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                   g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration the European the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-92344566; PubMed-1637296;
Hubner S., Michel F., Rudloff V., Appelhans H.;
Ergequence of band-3 protein from rainbow trout
erythrocytes derived from CDNA.";
Blochem. J. 285:17-23(1992).

-1 FUNCTION: BAND 3 HAS TWO FUNCTIONAL DOMAINS: ITS INTEGRAL DOMAIN
MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS THE MEMBRANE,
WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING SITES FOR
CYTOSKELETAL AND OTHER PROTEINS (BY SIMILARITY).

-1 SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY
AND APPEARS TO BE TETRAMERIC (BY SIMILARITY).

-1 SUBCELLULAR LOCATION: Integral membrane protein.
-1 SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane; Glycoprotein; Anion exchange; Lipoprotein; Palmitate.

L 392 CYTOPLASMIC (POTENTIAL).

DOMAIN 393 918 MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (PROBABLE).
; FF4ECAD6D60CF0CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                   Score 100; DB 1; Length 922;
Pred. No. 2e-08;
  EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                        CYTOPLASMIC (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           918 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00219; ANION_EXCHANGER_1; 1. PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                        POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP, P02730; 1BTQ.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00955; HCO3_cotransp; 1. PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                 102223 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1993 (Rel. 27, Created)
01-FEB-1996 (Rel. 33, Last sequ
15-JUL-1999 (Rel. 38, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Band 3 anion exchange protein
                                                                                                                                                                                                                                                                                                                                                                         96.2%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X61699; CAA43868.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                               18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGRFAMS; TIGR00834; ae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                     635
671
691
730
791
817
817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S24318; S24318.
                                                                                                                                                                                                                                                                                                                    922 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLC4A1 OR AE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B3AT_ONCMY
P32847;
                                                        DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                         TRANSMEM
CARBOHYD
                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                           TRANSMEM
                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                        TRANSMEM
                                                                                                                DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B3AT_ONCMY

JC B3AT_OLOGY

DT 01-PEB

DT 01-PEB

DT 01-SC4A1

OS SC4A1

OS CACTINO

OC ACTINO

OC ACTINO

OC ACTINO

OC ACTINO

CC A
                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
834444444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Stomach;
MEDILINE-90094439; PubMed-2294114;
Rudrycki K.E., Newman P.R., Shull G.E.;
Rudrycki K.E., Newman G.E.;
Figh closing and tissue distribution of mRNAs for two proteins that are related to the band 3 Cl-/HCO3-exchanger.";
J. Biol. Chem. 265:462-471(1990).
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anlon exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
SLC4A2 OR AE2 OR B3RP2.
                                                                                                                                                                                                                              N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
'; 37E163141FBDC16A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kopito 1R.R.;
"Functional expression and subcellular localization of an anion exchanger cloned from choroid plexus.";
Proc. Natl. Acad. Sci. U.S.A. 87:5278-5282(1990).
-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE DISTRIBUTION.
                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-90319095; PubMed-2371270;
Lindsey A.E., Schneider K., Simmons D.M., Baron R., Lee B.S.,
                                                                                                                                                                                                                                                                                    Score 95; DB 1; Length 918;
Pred. No. 1.3e-07;
Mismatches 1; Indels
                                                                    EXOPLASMIC LOOP (POTENTIAL)
                                                                                                              POTENTIAL. EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                                                 PALMITATE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                  POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1234 AA.
                                                                                                                                                                                                                                                                                                                   1; Mismatches
             POTENTIAL
                                                          POTENTIAL
                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                     POTENTIAL
                                           POTENTIAL
                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                            1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                           101893 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                       91.3%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; J05166; AAA40799.1; -.
                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat)
                                                                                                                                                                                                                                            568
918 AA;
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
                                                                                                                                                                                   794
853
852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rrssue=Brain;
                                                                                  TRANSMEM
DOMAIN
                                                                                                                                           TRANSMEM
TRANSMEM
                                                                                                                                                                                    TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                            CARBOHYD
SEQUENCE
TRANSMEM
                                                       TRANSMEM
                                                                                                             TRANSMEM
                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                 B3A2_RAT
                                                                                                                                                                        TRANSMEM
             FRANSMEM
                             TRANSMEM
                                         PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                    B3A2_RAT
ò
                                                                                                                                                                                                                                                                                                                                                                         g
```

```
Name-B1;
                                                                                                                                                                                     Name-C1;
                                                                                                                                                   Name-B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIPID
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1237 AA.
P13808; 095809; 095810; 095811; 095812; 095813;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
SIC4A2 OR AE2
MUSS musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM A).

MEDLINE-88034212; Pubmed-3182834;

Alper S.L., Kopito R.R., Libresco S.M., Lodish H.F.;

"Cloning and characterization of a murine band 3-related cDNA from kidney and from a lymphoid cell line.";

Y. Biol. Chem. 263:17092-17099(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY. MEDLINE-20462926; Pubmed-11006093; Lecanda J., Urtasun R., Medina J.F.; Medina J.F.; Medina J.F.; Mojecular cloning and genomic organization of the mouse AE2 anion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                 !ransmembrane; Glycoprotein; Transport; Antiport; Ion transport;
\u00e4nion exchange; Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 93; DB 1; Length 1234; Pred. No. 3.7e-07;
                                                                                                                                                                                                                                                                 POTENTIAL.
EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                  HIS-RICH.

N-LINKED (GLCNAC. . .) (POTE N-LINKED (GLCNAC. . .) (POTE N-LINKED (GLCNAC. . .) (FOTE PALMITATE (BY SIMILARITY).

G -> A (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; · Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136635 MW; FAB4ED12BB916216 CRC64;
                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
MEMBRANE (ANION EXCHANGE)
                                                                                                                                                                                                                                                                                                 POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31ochem. Biophys. Res. Commun. 276:117-124(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -> I (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL. POTENTIAL.
                         InterPro; IPR001717; Anion_exchange.
InterPro; IPR0013020; HC03_cotranspt.
Pfam; PF00955; HC03_cotranspt.
PRINTS; PF001231; HC03TRNSPORT.
TIGREAMS; TIGR00834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                     PRO-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RR -> PG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.4%;
85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 85.0
17; Conservative
PIR; A34911; A34911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                  Anion exchange;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exchanger
                                                                                                                                                                                                                                                TRANSMEM
TRANSMEM
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                 DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                   PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                 FRANSMEN
                                                                                                                                                                                                                                                                                                                                               TRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                    RANSME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                   OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ID DTT ACCOUNT OF THE SECTION OF THE
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                            Isoid-P13808-5; Sequence-VSP_000459, VSP_000461;
-! TISSUE SPECIFICITY: Isoform a is widely expressed at similar levels in all tissues examined. Isoforms bl and b2 are predominantly expressed in stomach although they are also detected at lower levels in other tissues. Isoform c1 is stomach-specific. Isoform c2 is expressed at slightly higher levels in lung and stomach than in other tissues.
-! SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -> MDFLLRPQ (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane; Glycoprotein; Transport; Antiport; Ion transport; Anion exchange; Lipoprotein; Palmitate; Alternative splicing. DOMAIN 1 CYTOPLASMIC (POTENTIAL) DOMAIN 704 1237 MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . .) (POTENTIAL). . .) (POTENTIAL). . .) (POTENTIAL).
     WIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
EXOPLASMIC LOOP (POTENTIAL)
POTENTIAL.
  ΟF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (F
PALMITATE (BY SIMILARITY)
MSSAPRRPASGADSLHT -> MDFI
FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL). POTENTIAL).
                                                      SUBCELLULAR LOCATION: Integral membrane protein. ALTERNATIVE PRODUCTS:
                                                                                                         Event-Alternative splicing; Named isoforms-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B2).
/FTId=VSP_000457
                                                                                                                                                                                                                   IsoId = P13808-2; Sequence = VSP _ 000458;
                                                                                                                                                                                                                                                                            IsoId=P13808-3; Sequence=VSP_000457;
                                                                                                                                                                                                                                                                                                                               IsoId-P13808-4; Sequence-VSP_000460;
                                                                                                                                                            IsoId-P13808-1; Sequence-Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGREAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF255774; AAG23158.1; --
EMBL; AF255774; AAG23158.1; --
EMBL; AF255774; AAG23157.1; --
EMBL; AF255774; AAG23157.1; --
HSSP; P02730; 1BTO.
MGD; MGI:109351; Slc4a2.
InterPro; IPR0001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotranspt.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AF255774, AAG23154.1,
EMBL, AF255774, AAG23155.1,
EMBL, AF255774; AAG23155.1,
EMBL, AF255774; AAG23156.1,
EMBL, AF255774; AAG23156.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; J04036; AAA65505.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1237
727
770
```



GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein . protein search, using sw model

September 3, 2003, 11:25:42; Search time 9.25 Seconds (without alignments) 101.679 Million cell updates/sec Run on:

US-10-087-464-2 98 1 SVTHANALTVMGKASTPGAA 20 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

127863 Total number of hits satisfying chosen parameters:

127863 seqs, 47026705 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	P02730 homo sapien	2 rattu	_			_		homon	gallu	oncorhy	P16283 mus musculu	P23348 rattus norv		_			P14914 rickettsia	Q53047 r outer mem	P19338 homo sapien				Q8uey3 agrobacter1		P33025 escherichia	Q92210 candida alb	Q10821 mycobacteri	Q61140 mus musculu				P29118 cephalospor	-
CHANAMACC	ID	B3AT_HUMAN	B3AT_RAT	B3AT_MOUSE	B3A2_RAT	B3A2_MOUSE	B3A2_RABIT	B3A2_CAVPO	B3A2_HUMAN	B3AT_CHICK	B3AT_ONCMY	B3A3_MOUSE	B3A3_RAT	B3A3_HUMAN	B3A3_RABIT	Y003_HAEIN	OMPB_RICCN	120K_RICRI	OMPB_RICRI	NUCL_HUMAN	FTSY_RICPR	WD21_HUMAN	YFC5_SHEFR	TPIS_AGRT5	PANB_OCEIH	YEIN_ECOLI	PUR6_CANAL	- 1	BCA1_MOUSE	BCA1_RAT	ο.	BRS3_MOUSE	ALP_CEPAC	OPS4_CANAL
	DB	-	~	-	,-	Н	Н	-	Н	-	-	٦	٦	-	-	-	-	-	~	, ,	-	-	-	~	-4	-	-	П	-	.	-4	-	-	1
	Length	911	927	929	1234	1237	1237	1238	1241	922	918	1227	1227	1232	1233	262	1655	1300	1654	106	303	495	122	256	270	312	268	779	874	896	190	399	402	402
	Ouery Match		5.9	•	•		٠	٠	5.5	٠	4 · 3	5.7	<u>رب</u>		?	0	0	0	0							æ ·								
æ	Mat		9,			7		7	7	-	9	9	9	6	9	ĭ,	4	₹.	₹.	4	4	4	4	4	4	40	4	40	7	40	5	m m	8	30
	Score	86	91	91	73	73	73	73	73	7.1	63	61	61	61	61	40	*	47	- 1	42.5	42	41.5	41	41	40	40	40	04.	04	40		9.5		
	Result No.	1	7	m	4	S	9	7	Φ.	σ,	10	Ξ:	12	ET :	14	15	91	17	80	61	20	21	22	23	24	25	56	77	87	57	9.0	T :	32	33

Q11178 caenorhat 005049 xenopus 1	064336 mus muscu 016650 homo sapi	Q16799 homo sap	Q15782 homo sapi P52441 human her	004475 brachydanio 0920v8 rickettsia	09zcs7 rickettsi P94368 bacillus	
YPC1_CAEEL MUC1_XENLA	TBR1_MOUSE	RTN1_HUMAN EGSA_METAC	C3L2_HUMAN	B2MG_BRARE RS13 RICCN	RS13_RICPR YXKO_BACSU	
	1				п п	
529 662	681 682	776 356	390	116	125 276	
39.8 39.8	39.8 39.8	39.8	90.9	38.8	38.8 38.8	
36 36 36	39 39	39 38.5	38.5	38	38 38	
34 35	36 37	38 36	40	4 4 8	44 45	

ALIGNMENTS

RESULT 1

```
PHOSPHORYLATION OF TYR-8; TYR-21; TYR-359 AND TYR-904.
MEDLINE-20400020; Pubbed=10942405;
Brunati A.M., Bordin L., Clari G., James P., Quadroni M., Baritono E., Pina L.A., Donella-Deana A.;
"Sequential phosphorylation of protein band 3 by Syk and Lyn tyrosine Kinases In intact human erythrocytes: identification of primary and secondary phosphorylation sites.";
Blood 96:1550-1557(2000).
                                                                                                                                                                                                       Kawano Y., Okubo K., Tokunaga F., Miyata T., Iwanaga S., Hamasaki N.; "Localization of the pyridoxal phosphate binding site at the COOH-terminal region of erythrocyte band 3 protein."; J. Biol. Chem. 263:823-8238(1988).
             conformation and a possible molecular mechanism for anion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-92107882; PubMed-1722314; Jacolim P., Sapak P., Nurse G.T., Rubin H.L., Zhai S., Sahir K.E., Liu S.-C.; Pablir K.E., Liu S.-C.; Deletion in erythrocyte band 3 gene in malaria-resistant Southeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT HE 400-ALA--ALA-408 DEL.
MEDLINE-92167271; PubMed=1538405;
Schoffeld A.E., Tanner M.J.A., Pinder J.C., Clough B., Bayley P.M.,
Nash G.B., Dluzewski A.R., Reardon D.M., Cox T.M., Wilson R.J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Okubo K., Hamasaki N., Hara K., Kageura M.; Palmitoylation of cysteine 69 from the COOH terminal of band 3 protein in the human erythrocyte membrane. Acylation occurs in the middle of the consensus sequence of F-I-IICLANL found in band 3 protein and G2 protein of Rift Valley fever virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Band 3 Tuscaloosa: Pro-327-->Arg substitution in the cytoplasmic domain of erythrocyte band 3 protein associated with spherocytic hemolytic anemia and partial deficiency of protein 4.2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-91329825; PubMed-1678289;
Yannoukakos D., Vasseur C., Driancourt C., Blouquit Y., Delauney Wajcman H., Bursaux E.;
"Human erythrocyte band 3 polymorphism (band 3 Memphis):
characterization of the structural modification (Lys 56-->Glu) by protein chemistry methods.";
Blood 78:1117-1120(1991).
                                                                                                                                                                                                                                                                                                                                                                           ROLE OF GLU-681, AND SEQUENCE OF 665-688.
MEDLINE-92332495; PubMed-1352774;
Jennings M.L., Smith J.S.;
"Anion-proton cotransport through the human red blood cell band protein. Role of gliutemate 681.";
J. Biol. Chem. 267:13964-13971(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT HE 400-ALA--ALA-408 DEL, AND VARIANT MEMPHIS GLU-56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT HS ARG-327.
MEDLINE-92329950; PubMed-1378323;
Jarolim P., Palek J., Rubin H.L., Prchal J.T., Korsgren C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Basis of unique red cell membrane properties in hereditary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 88:11022-11026(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein and G2 protein of Rift Valley
J. Biol. Chem. 266:16420-16424(1991).
                                                                                                                                                                           MEDLINE-88228050; PubMed-3372523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91358422; PubMed=1885574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARÍANT HS LEU-868.
MEDLINE-93343855; PubMed-8343110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ovalocytosis.";
J. Mol. Biol. 223:949-958(1992)
                                                                            Blochem. J. 213:577-586(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PALMITOYLATION OF CYS-843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT MEMPHIS GLU-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blood 80:523-529(1992)
                                                                                                                                               SEQUENCE OF 834-911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Asian ovalocytosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gratzer W.B.;
sednence, c
                                             exchange.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cohen C.
          REAL TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND SECO
```

```
VARIANTS HS GLN-760; TRP-760; CYS-808 AND TRP-870.
MEDLINE-95134893; PubMed=753050;
Jarolim P., Rubin H.L., Brabec V., Chrobak L., Zolotarev A.S.,
Alper S.L., Brugnara C., Wichterle H., Palek J.;
"Mutations of conserved arginines in the membrane domain of erythroid band 3 lead to a decrease in membrane-associated band 3 and to the phenotype of herealtary spherocytosis.";
                                                                                                                                                                                                        "Human erythrocyte protein 4.2 deficiency associated with hemolytic anemia and a homozygous 40 glutamic acid-->lysine substitution in the cytoplasmic domain of band 3 (band 3Montefiore).";
Bruce L.J., Kay M.M., Lawrence C., Tanner M.J.; "Band 3 HT, a human red-cell variant associated with acanthocytosis and increased anion transport, carries the mutation Pro-868-->Leu in the membrane domain of band 3."; Biochem. J. 293:317-320(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bozon M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT HS ASP-771.
MEDILER-961316073; PubMed-8547122;
Maillet P., Vallier A., Reinhart W.H., Wyss E.J., Ott P., Texier P.,
Baklouti F., Tanner M.J., Delaunay J., Alloisio N.;
"Band 3 Chur: a variant associated with band 3-deficient hereditary
spherocytosis and substitution in a highly conserved position of
transmembrane segment 11.";
                                                                                                                                                                                                                                                                                                            VARIANT BLOOD GROUP DI(A)/MEMPHIS-II.
MEDLINE=94266802; PubMed=8206915;
Bruce L.J., Anstee D.J., Spring F.A., Tanner M.J.;
Band 3 Memphis variant II. Altered stilbene disulfonate binding a the Diego (Dia) blood group antigen are associated with the human erythrocyte band 3 mutation Pro-854-->Leu.";
J. Blol. Chem. 269:16155-16158(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Changes in the blood group Wright antigens are associated with a mutation at amino acid 658 in human erythrocyte band 3: a site of interaction between band 3 and glycophorin A under certain conditions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANTS HS LYS-40; CYS-518 AND MET-663 DEL.
MEDLINE-96225450; PubMed-8640229;
EDER S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,
Dornwell M., Herbers J., Kugler W., Oezcan R., Pekrun A.,
Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;
Annyrin -1 mutations are a major cause of dominant and recessive harad4+ary cahberocutes ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-97351102; PubMed-9207478;
Alloisio N., Texier P., Vallier A., Ribeiro M.L., Morle L., Bozor
Bursaux E., Maillet P., Goncalves P., Tanner M.J., Tamagnini G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Characterization of 13 novel band 3 gene defects in hereditary spherocytosis with band 3 deficiency.", Blood 88:4366-4374(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jarolim P., Murray J.L., Rubin H.L., Taylor W.M., Prchal J.T., Ballas S.K., Snyder L.M., Chrobak L., Melrose W.D., Brabec V.,
                                                                                                                                           MEDLINE-93229758; PubMed-8471774;
Rybicki A.C., Qiu J.J.H., Musto S., Rosen N.L., Nagel R.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANTS HS ASP-285; GLU-455; PRO-707; PRO-834 AND MET-837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reid M.E., Wilkinson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT BLOOD GROUP WR(A).
MEDLINE-95111140; PubMed-7812009;
Bruce L.J., Ring S.M., Anstee D.J.,
Tanner M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Haematol, 91:804-810(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97099297; PubMed=8943874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANTS HS SER-147 AND MET-488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hereditary spherocytosis.";
Nat. Genet. 13:214-218(1996).
                                                                                                                                                                                                                                                                       Blood 81:2155-2165(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blood 85:541-547(1995).
                                                                                                                         VARIANT MONTEFICRE
                                                                                                                                                                                      Schwartz R.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Palek J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           [18]
```

```
KKK
KELLILIKE KELLI
KELLIKE KELLIKE KELLI
KELLIKE KKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --- FUNCTION: BAND 3 HAS TWO FUNCTIONAL DOMAINS: ITS INTEGRAL DOMAIN HEDTATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS THE MEMBRANE, WHEREAS ITS CYTOGRELETAL MED FOUNDES BINDING SITES FOR CYTOGRELETAL AND OTHER PROTEINS (BY SIMILIARITY)
--- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY AND APPEARS TO BE TETRAMERIC.
--- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. IN THE BASOLATERAL MEMBRANE OF INTERCALATED CELLS OF DISTAL TUBULES AND COLLECTING DUCTS.
                                                                 Gaps
                                                                                                                                                                                                                                                                                                               01-NOV-1991 (Rel. 20, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
SLC4A1 OR AEI.
Rattus norvegicus (Rat).
ENBATYOCA3 Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kudrycki K.E., Shull G.E.;
Prihary structure of the rat kidney band 3 anion exchange protein
deduced from a cDNA.";
J. Biol. Chem. 264:8185-8192(1989).
                                                               ö
                Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGREAMS; TIGRO0884; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;
                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kudrycki K.E., Shull G.E.;
Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isoid=P23562-2; Sequence=VSP_000455;
TISSUE SPECIFICITY: Kidney.
SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
                Score 98; DB 1;
Pred. No. 1.5e-08;
                                                                                                                                                                                                                                                                     927 AA.
                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=Erythrocyte;
IsoId=P23562-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; J04793; AAA40800.1; ALT_INIT
                                                                                                                                MEDLINE-89255254; \PubMed-2722777;
                                                                                                        1 SVTHANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00955; HCO3_cotransp; 1.
PRINTS; PR01231; HCO3TRNSPORT.
              100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 46-927 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L02943; AAA40801.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-45 FROM N.A.
            Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A33810; A33810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Kidney
                                                                                                                                                                                                                                                                   B3AT_RAT
P23562;
                                                                                                          ò
                                                                                                                                                   g
                                                                                                                                                                                                                                                                          AND DE REPRESENTATION OF THE PROPERTY OF THE P
```

```
Kopito R.R., Lodish H.F.; "Primary structure and transmembrane orientation of the murine anion exchange protein."; Nature 316:234-238(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse),
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Band 3 anion transport protein (Anion exchange protein 1) (AE 1)
                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (PROBABLE).
PALMITATE (BY SIMILARITY).
Missing (in isoform Kidney).
                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                           Length 927;
                                                                                                                                                                                     POTENTIAL. EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                                     EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARTIAL SEQUENCE FROM N.A.
MEDLINE-87250387; Pubmed-3036795;
Kopito R.R., Andersson M., Lodish H.F.;
"Structure and organization of the murine band 3 gene.";
J. Biol. Chem. 262:8035-8040(1987).
                CYTOPLASMIC (PÔTENTIAL).
MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUL-1987) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                      681A228474E5E9DE CRC64;
                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-86034211; PubMed-3840489;
Kopito R.R., Lodish H.F.;
"Structure of the murine anion exchange protein.";
J. Cell. Blochem. 29:1-17(1985).
                                                                                                                                                                                                                                                                                                                                                                                                           Score 91; DB 1; I
Pred. No. 2.2e-07;
                                                                                                                                                                                                                                                                                                                                                           000455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   929 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVTHANALTVMGKASGPGAA 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE-85268011; Pubmed-2410791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 11-929 FROM N.A. MEDLINE-86274622; PubMed-3015590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SVTHANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                           MW.
                                                                                                                                                                                                                                                                                                                                                                                                          92.9%;
95.0%;
                                                                                                                                                                                                                                                                                                                                                                         103172
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
Lipoprotein; Palmitate;
                                                441
4473
4473
527
558
5604
619
                                                                                                                                                                                                    676
696
735
822
881
859
79
                                                                                                                                                                                                                                                                                                                                                                         927 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity
Matches 19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                   559
585
605
620
641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLC4A1 OR AE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B3AT_MOUSE
P04919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             747
                                DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                     TRANSMEM
                                                                                                                                                                                     PRANSMEM
                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                   PRANSMEM
                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                       PRANSMEM
                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                         VARSPLIC
                                                                 PRANSMEM
                                                                                   FRANSMEM
                                                                                                   FRANSMEN
                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                     DOMAIN
                                                                                                                                     DOMAIN
                                                                                                                                                                                                       DOMAIN
```

·:

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

September 3, 2003, 11:25:42 ; Search time 9.25 Seconds
(without alignments)
101.679 Million cell updates/sec Run on:

US-10-087-464-3 96 1 GRASTPGAAAQIQEVKEQRI 20 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

•	Description	P02730 homo sapien	rattu	<u>-</u>	_	7 rattus	mus mus	-			_	P23348 rattus norv		-		Sdwnw		Q63083 rattus norv		-		O13923 schizosacch	٠.			P31168 arabidopsis		Q81999 human papil	_	28	S	6	5	P30848 escherichia
SUMMAKIES	DI	B3AT_HUMAN	B3AT_RAT	B3AT_MOUSE	B3AT_CHICK	B3A2_RAT	B3A2_MOUSE	B3A2_RABIT	B3A2_CAVPO	B3A2_HUMAN	B3A3_MOUSE	B3A3_RAT	B3A3_HUMAN	B3A3_RABIT	RRPP_MUMPE	RRPP_MUMPM	NCB1_MOUSE	NCB1_RAT	NCB1_HUMAN	RLOC_ARATH	YDJE_ECOLI	CORO_SCHPO	YNQ6_YEAST	CAC2_HAECO	BASP_RAT	DH47_ARATH	FOJO_DROME	VE1_HPV72		VIL1_MOUSE	IF2_LACLC	- 1		PROP_ECOLI
	DB	-	٦	Н	Н	-	-	-	-			-	,	-	-	П	-	٦	<u>, , , , , , , , , , , , , , , , , , , </u>	- -4	-	н,	٠,	,	- 1 ·	-	Н,	-	⊶,	⊣,	-	н.	Η,	-
	Length	911	927	929	922	1234	1237	1237	1238	1241	1227	1227	1232	1233	391	391	459	459	461	323	452	601	448	210	219	265	583	650	826	826	950	2116	2418	200
ap (Match	0	92.7	$^{\circ}$	63.5	v	v	•	0	·.	٠	٠.	٠.	٠.	٠.	٠.	5	•		٠	₹.	44.8	٠,	42.7	٠,	· i	42.7	42.7	· in	42.7		42.7	42.7	47.7
	Score	96	89	68	61	28	28	28	28	28	54	54	54	54	45		44	44	44	4.	43	4 E. (7.	41	7:	4.1	41	7	41	4.1	41	41	•	40.0
+ 1.000	NO.	1	7	m	∢	w.	9	7	ω (σ,	10	11	12	13	†T	15	16	17	18	6T	20	21	77	573	7 0	572	50	17	87	67	200	4.5	3.5	.

P40862 salmonella				-		P46466 oryza sativ	Q929c8 chlamydia p	09s487 prochloroco	Q50329 mycoplasma			
PROP_SALTY	PKP1_MOUSE	RL7_ANASP	HAP3_YEAST	RK12_TOBAC	BCHN_CHLAU	PRS4_ORYSA	RADA_CHLPN	DNAA_PROS9	ATPA_MYCPN	CIK1_YEAST	UL93_HCMVA	
7	Н	-	П	_	٦	7	_	Н	Н	-	Т	
200	728	129	144	186	444	448	453	463	518	594	594	
42.2	42.2	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	
40.5	40.5	40	40	40	40	40	40	40	40	40	40	
34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

RESULT 1

B3AT ID	BARTHUMAN BARTHUMAN STANDARD; PRT; 911 AA.
AC	
<u> </u>	21-JUL-1986 (Rel. Ol, Created) 01-APR-1990 (Rel. 14. Last semience undate)
D.T.	15-SEP-2003 (Rel. 42, Last annotation update)
DE	trans
E CE	
Z (SEC4AI OR AEL OR EPB3 OR DI.
3 5	
3 6	buvaijora, Marazdos, iloimatas, Cialistas (Victobrata) Eurotereoscomij Mammalja: Eurheria: Drimates: Catarrhini: Hominidae: Bome
ö	
RN	[1]
RP	SEOUENCE FROM N.A.
RX	MEDLINE=90083213; PubMed=2594752;
RA	Lodish
RT	band 3,
RT	
¥.	Proc. Nati. Acad. Sci. U.S.A. 86:9089-9093(1989).
Z C	
χ, t	SEQUENCE FROM N.A.
2 2	TINGUE BLOOM
X á	MEDDINE=891341/2; PubMed=32234/;
5 5	
7. T. T.	בר הסיד ליים ה
ET.	CHE COINA
RN	
RP	SEQUENCE OF 1-199: 220-292 AND 347-370.
RX	MEDLINE=90001294; PubMed=2790053;
RA	Yannoukakos D., Vasseur C., Blouguit Y., Bursaux E., Wajcman H.;
RŢ	domain of human erythro
RŢ	protein band 3. Comparison with its sequence in the mouse.";
RL	Biochim. Biophys. Acta 998:43-49(1989).
RN	[4]
RP	SEQUENCE OF 1-201.
XX	MEDLINE=83238395; PubMed=6345535;
KA I	Kaul K.K., Murthy S.N.P., Reddy A.G., Steck T.L., Kohler H.;
RI	"Amino acid sequence of the N alpha-terminal 201 residues of human
K.	erythrocyte membrane band 3.";
RI.	J. Biol. Chem. 258:7981-7990(1983).
KN	[2]
RP	SEQUENCE OF 1-3.
KX I	MEDLINE=79027186; PubMed=701248;
ΚA	Drickamer L.K.;
RŢ	"Orientation of the band 3 polypeptide from human erythrocyte
КŢ	membranes. Identification of NH2-terminal sequence and site of
RT	carbohydrate attachment.";
RL	J. Biol. Chem. 253:7242-7248(1978).
RN	
RР	SEQUENCE OF 559-630.
RX	MEDLINE=83308584; PubMed=6615451;
RA	Brock C.J., Tanner M.J.A., Kempf C.;
RŢ	"The human erythrocyte anion-transport protein. Partial amino acid

```
Brunati A.M., Bordin L., Clari G., James P., Quadroni M., Baritono E., Pinna L.A., Donella-Deana A.; "Sequential phosphorylation of protein band 3 by Syk and Lyn tyrosine kinases in intact human erythrocytes: identification of primary and secondary phosphorylation sites."; Blood 96:1550-1557(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT HE 400-ALA--ALA-408 DEL, AND VARIANT MEMPHIS GLU-56.
MEDITINE-92107882; PubMed-1722314;
Jarolim P., Palek J., Amato D., Hassan K., Sapak P., Nurse G.T.,
Rubin H.L., Zhai S., Sahr K.E., Liu S.-C.;
"Deletion in erythrocyte band 3 gene in malaria-resistant Southeast
   sequence, conformation and a possible molecular mechanism for anion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT HE 400-ALA--ALA-408 DEL.
MEDLINE-9212721; PubMed=1538405;
Schoffleld A.E., Tanner M.J.A., Pinder J.C., Clough B., Bayley P.M.,
Nash G.B., Dluzewski A.R., Reardon D.M., Cox T.M., Wilson R.J.M.,
Gratzer W.B.;
                                                                                                                                                                                                        Hamasaki N
                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-92332495; PubMed-1352774; Jennings M.L., Smith J.S.; Jannings M.L., Smith J.S.; Anion-proton cotransport through the human red blood cell band 3 protein. Role of glutemate 681."; J. Biol. Chem. 267:13964-13971(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Band 3 Tuscaloosa: Pro-327-->Arg substitution in the cytoplasmic domain of erythrocyte band 3 protein associated with spherocytic hemolytic anemia and partial deficiency of protein 4.2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Okubo K., Hamasaki N., Hara K., Kageura M.;
Palmitoylation of cysteine 69 from the COOH-terminal of band 3 protein in the human erythrocyte membrane. Acylation occurs in the middle of the consensus sequence of F-I-IICLAVL found in band 3 protein and G2 protein of Rift Valley fever virus.";
J. Biol. Chem. 266:16420-16424(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-91329825; PubMed-1678289;
Yannoukakos D., Vasseur C., Driancourt C., Blouquit Y., Delauney, Wajcman H., Bursaux E.;
"Human erythrocyte band 3 polymorphism (band 3 Memphis):
characterization of the structural modification (Lys 56-->Glu) by profein chemistry methods.";
plood 78:1117-1120(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Basis of unique red cell membrane properties in hereditary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-92329950; PubMed-1378323;
Jarolim P., Palek J., Rubin H.L., Prchal J.T., Korsgren C.
                                                                                                                                                           MEDLINE-88228050; PubMed-3372523; Kawano Y., Okubo K., Tokunaga F., Miyata T., Iwanaga S., Localization of the pyridoxal phosphate binding site at terminal region of erythrocyte band 3 protein."; J. Biol. Chem. 263:8232-8238(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION OF TYR-8; TYR-21; TYR-359 AND TYR-904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Asian ovalocytosis.";
Proc. Natl. Acad. Sci. U.S.A. 88:11022-11026(1991).
                                                                                                                                                                                                                                                                                                                                                                   ROLE OF GLU-681, AND SEQUENCE OF 665-688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20400020; PubMed=10942405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PALMITOYLATION OF CYS-843.
MEDLINE-91358422; PubMed-1885574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mol. Biol. 223:949-958(1992)
                                                                 Blochem. J. 213:577-586(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT MEMPHIS GLU-56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lood 80:523-529(1992)
                                                                                                                                   SEQUENCE OF 834-911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HS ARG-327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT HS LEU-868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ovalocytosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cohen C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT
THE SECTION OF THE SE
```

MEDLINE-93343855; PubMed-8343110;

```
VARÍANTS HS GLN-760; TRP-760; CYS-808 AND TRP-870.
MEDLINE-95134983; PubMed=7530501;
Jarolim P., Rubin H.L., Brabec V., Chrobak L., Zolotarev A.S.,
Alper S.L., Brugnara C., Wichterle H., Palek J.;
"Mutations of conserved arginines in the membrane domain of erythroid band 3 lead to a decrease in membrane-associated band 3 and to the phenotype of hereditary spherocytosis.";
                                                                                                                                                                                                            "Human erythrocyte protein 4.2 deficiency associated with hemolytic anemia and a homozygous 40 glutamic acid-->lysine substitution in the cytoplasmic domain of band 3 (band 3Monteficre)."; also 31:2155-2165(1993).
                                                                                                                                                                                                                                                                                                                                          MEDLINE-94266802; PubMed-6206915;
Bruce L.J., Anstee D.J., Spring F.A., Tanner M.J.;
Bruce L.J., Anstee D.J., Spring F.A., Tanner M.J.;
"Band 3 Memphis variant II. Altered stilbene disulfonate binding and the Diego (Dia) blood group antigen are associated with the human erythrocyte band 3 mutation Pro-854-->Leu.";
J. Biol. Chem. 269:16155-16158(1994).
Bruce L.J., Kay M.M., Lawrence C., Tanner M.J.; "Band 3 HT, a human red-cell variant associated with acanthocytosis and increased anion transport, carries the mutation Pro-868-->Leu in the membrane domain of band 3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bozon M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT HS ASP-771.
MEDLINE-96136073; PubMed-8547122;
Maillet P., Vallier A., Reinhart W.H., Wyss E.J., Ott P., Texier P.,
Baklouti F., Tanner M.J., Delaunay J., Alloisio N.,
"Baklouti F., Tanner M.J., Delaunay J., Alloisio N.,
"Band 3 Chur: a variant associated with band 3-deficient hereditary spherocytosis and substitution in a highly conserved position of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Changes in the blood group Wright antigens are associated with a mutation at amino acid 658 in human erythrocyte band 3: a site of interaction between band 3 and glycophorin A under certain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T., Dornwell M., Herbers J., Kugler W., Oezcan R., Pekrun A., Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.; Ankyrin-1 mutations are a major cause of dominant and recessive hereditary sobercetes ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alloisio N., Texier P., Vallier A., Ribeiro M.L., Morle L., Bozon
Bursaux E., Maillet P., Goncalves P., Tanner M.J., Tamagnini G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Characterization of 13 novel band 3 gene defects in hereditary spherocytosis with band 3 deficiency."; Blood 88:4366-4374(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jarolim P., Murray J.L., Rubin H.L., Taylor W.M., Prchal J.T., Ballas S.K., Snyder L.M., Chrobak L., Melrose W.D., Brabec V.,
                                                                                                                              VARIANT MONTEFIORE LYS-40.

BEDLINE-33229788; PubMed-8471774;

Rybicki A.C., Qiu J.J.H., Musto S., Rosen N.L., Nagel R.L., Schwartz R.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANTS HS ASP-285; GLU-455; PRO-707; PRO-834 AND MET-837.
MEDLINE-97099297; Pubmed-8943874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT BLOOD GROUP WR(A).
MEDLINE-95111140; PubMed-7812009;
Bruce L.J., Ring S.M., Anstee D.J., Reid M.E., Wilkinson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANTS HS LYS-40; CYS-518 AND MET-663 DEL. MEDLINE-96225450; Pubmed-8640229;
                                                                                                                                                                                                                                                                                                                        VARIANT BLOOD GROUP DI(A)/MEMPHIS-II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transmembrane segment 11.";
Br. J. Haematol, 91:804-810(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97351102; PubMed-9207478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANTS HS SER-147 AND MET-488
                                                                                   Biochem. J. 293:317-320(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hereditary spherocytosis,";
Nat. Genet. 13:214-218(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blood 85:541-547(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fanner M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Palek J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13
```

~

```
RESULT 3
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1991 (Rel. 20, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Band 3 anion transport protein (Anion exchange protein 1) (AE 1).
SLC4A1 OR AE1.
                                                                  ö
            100.0%; Score 96; DB 1; Length 911; 100.0%; Pred. No. 2.6e-07; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY: Kidney.
SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event-Alternative splicing; Named isoforms-2;
                                                                                                                                                                                                                                                                           927 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=P23562-2; Sequence=VSP_000455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P23562-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HC03_cotranspt.
Pfam; PF00955; HC03_cotransp; 1.
PRINTS; PR01231; HC03TRNSPORT.
TIGRFAMS; TICR00834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                deduced from a cDNA.";
J. Blol. Chem. 264:8185-8192(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; J04793; AAA40800.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Kidney;
MEDLINE-89255254; PubMed-2722777;
                                                                                                                                      1 GKASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L02943; AAA40801.1; -. PIR; A33810; A33810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 46-927 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-45 FROM N.A.
         Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name-Erythrocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name-Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP;
                                                                                                                                                                                                                          RESULT 2
                                                                                                                                                                                                                                                     B3AT_RAT
                                                                                                           á
                                                                                                                                                   q
                                                                                                                                                                                                                                                                                            A PART OF THE PROPERTY OF THE PROPERTY OF THE PART OF
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-85268011; PubMed-2410791;
Kopito R.R., Lodish H.F.;
"Primary structure and transmembrane orientation of the murine anion exchange protein.";
Nature 316:234-238(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Band 3 anion transport protein (Anion exchange protein 1) (AE 1)
                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. . .) (PROBABLE). PALMITATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                     Length 927;
                                                                                            POTENTIAL. EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                                                                EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                                                                                                                                                                             Missing (in isoform Kidney)./FTId=VSP_000455.
                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene.";
                                                                                                                                                                                                                                                                                                        681A228474E5E9DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUL-1987) to the EMBL/GenBank/DDBJ databases
             CYTOPLASMIC (POTENTIAL).
MEMBRANE (ANION EXCHANGE)
                                                                                                                        POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=86034211; PubMed=3840489;
Kopito R.R., Lodish H.F.;
"Structure of the murine anion exchange protein.";
J. Cell. Biochem. 29:1-17(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-87250387; PubMed-3036795;
Koptto R.R., Andersson M., Lodish H.F.;
"Structure and organization of the murine band 3
J. Blol. Chem. 262:8035-8040(1987).
                                                                                                                                                                                                                                                                                                                                                  3.4e-06;
                                                                                                                                                                                                                                                                                                                                     DB 1;
  splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         929 AA
                                                                                                                                                                                                                                                                                                                                                  Pred. No. 3.46
0; Mismatches
                                                    POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                          POTENTIAL. POTENTIAL.
                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                     Score 89;
 Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                         [5]
SEQUENCE OF 11-929 FROM N.A.
MEDLINE-86274622; Pubmed-3015590;
                                                                                                                                                                                                                                                                                                                                                                                          1 GKASTPGAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                  92.7%;
95.0%;
                                                                                                                                                                                                                                                                                                         103172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    Query Match 92.7
Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
Palmitate;
                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (1)
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                          4421
4421
4421
5508
559
559
6620
641
                                                                                                                                                                                          715
                                                                                                                                                                                                                                                                                                        927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MEB3).
SLC4Al OR AE1.
 Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B3AT_MOUSE
P04919;
                          DOMAIN
TRANSMEM
TRANSMEM
                                                                               TRANSMEM
TRANSMEM
                                                                                                                                      DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                             VARSPLIC
                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                         PRANSMEM
                                                                                                                                                                                                                                                   CARBOHYD
                                                                  TRANSMEM
                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                          FRANSMEM
                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                       TRANSMEM
                                                                                                           DOMAIN
                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kopito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B3AT_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MEB3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11D
DACODO OCCOO OCCO
```

.; 0

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

September 3, 2003, 11:25:42 ; Search time 9.25 Seconds
(without alignments)
101.679 Million cell updates/sec Run on:

US-10-087-464-4 112 1 DRILLLFKPPKYHPDVPYVK 20 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

127863 Total number of hits satisfying chosen parameters: 127863 seqs, 47026705 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	PO2730 homo sabien	rattu	PO4919 mus musculu		rattus	mus mus	P48746 oryctolagus			mus m	P23348 rattus norv				Q96dt0 homo sapien	m snm	_			Q64685 mus musculu		Q9fwk4 oryza sativ	-						P15907 homo sapien	_	al	609	112
SUMMARIES	ID	B3AT_HUMAN	B3AT_RAT	B3AT_MOUSE	B3AT_CHICK	B3A2_RAT	B3A2_MOUSE	B3A2_RABIT	B3A2_HUMAN	B3A2_CAVPO	B3A3_MOUSE	B3A3_RAT	B3A3_HUMAN	B3A3_RABIT	SOC7_HUMAN	LEGC_HUMAN	SOC7_MOUSE	B3AT_ONCMY	UL16_EBV	PPAF_ARATH	SIA1_MOUSE	WBP1_MOUSE	CYNS_ORYSA		VNS3_AHSV1	VNS3_AHSV2	VNS3_AHSV8	- 1	SIA1_RAT			DNLI_THEVO	DM3B_MOUSE	Y458_ANASP
	DB	-	-	-	Н		П	-	-	-	-	-		-		-	-	-	-4	-	-	-	~	-	-	1	⊶.	-	.	-	-		-	-
	Length	911	927	929	922	1234	1237	1237	1241	1238	1227	1227	1232	1233	440	336	436	918	336	469	403	304	168	234	218	218	218	578	403	406	434	588	859	179
œ	Query Match		96.4	96.4	73.2	66.1	66.1	66.1	66.1	65.2	60.7	60.7	٠			46.4	44.6	÷.	m.	m,	ä	ς.	Ċ.	ς,	41.1	μ,	∹,	≓,	40.2		٠,	;	٠	
	Score	112	108	108	82	74	74	74	74	73	89	9	62	62	28	52	20	20	49	49	٦,	47.5	47	47	40	9.	4 .	4. O i	φ.				45	44
	Result No.	1	~	m	₹ 1	ın.	9	۲,	20 (on (0 :	1;	12	13	14 1	15	16	17	81.	616	20	21	22	2.5	4.0	57	9 10	70	97	67	3.0	3.1	32	33



	058094 methanococc	000024 agaricus bi	P70711 rattus norv	P21734 saccharomyc	000341 homo sapien	P81021 gallus gall	001197 gossvojum h	P06503 trichoplusi	012705 xestia c-ni	P38552 rattus norv	P50108 saccharomyc	Oguqq2 homo sapien
)												
	TKTN_METJA	PPO1 AGABI	UB5D_RAT	UBC1_YEAST	VGLN_HUMAN	VGLN_CHICK	E6 GOSHI	GRAN_GVIN	GRAN_GVXN	LEG4_RAT	MN10 YEAST	LNK_HUMAN
	Ч	Н	-	_	-	Н	~	Н	٦	7	-	1
	274	568	147	215	1268	1270	238	248	248	324	393	575
	39,3	39.3	38.8	38.8	38.8	38.8	38.4	38.4	38.4	38.4	38.4	38.4
	44	44	43.5	43.5	43.5	43.5	43	43	43	43	43	43
	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

```
sequence, conformation and a possible molecular mechanism for anion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT HE 400-ALA--ALA-408 DEL, AND VARIANT MEMPHIS GLU-56.
MEDLINE-92107882; PubMed=1722314;
Jarolim P., Palek J., Amato D., Hassan K., Sapak P., Nurse G.T.,
Rubin H.L., Zhai S., Sahr K.E., Liu S.-C.;
"Deletion in erythrocyte band 3 gene in malaria-resistant Southeast
Asian ovalocytosis.";
                                                                                                                                                                                                                                                                                                                                    Okubo K., Hamasaki N., Hara K., Kageura M.;
"Palmitoylation of cysteine 69 from the COOH-terminal of band 3 protein in the human erythrocyte membrane. Acylation occurs in the middle of the consensus sequence of F-I-IICLAVL found in band 3 protein and G2 protein of Rift Valley fever virus.";
J. Biol. Chem. 266:16420-16424(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schoffeld A.E., Tanner M.J.A., Pinder J.C., Clough B., Bayley P.M., Nash G.B., Dluzewski A.R., Reardon D.M., Cox T.M., Wilson R.J.M.,
                                                                   SEQUENCE OF 834-911.

MEDLINE-88228050; PubMed-3372523;

MEDLINE-80228050; PubMed-3372523;

MEDLINE-80228050; PubMed-3372523;

Miyata T., Iwanaga S., Hamasaki hawano K., Tokunaga F., Miyata D., Iwanaga S., Hamasaki harlocalization of the pyridoxal phosphate binding site at the COOH-terminal region of erythrocyte band 3 protein.";

J, Blol. Chem. 263:8232-8238(1988).
                                                                                                                                                                                                                  Jennings M.L., Smith J.S.; "Anion-proton cotransport through the human red blood cell band 3 protein. Role of glutamate 681."; J. Biol. Chem. 267:13964-13971(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain of errithrocyte band 3 protein associated with spherocytic hemolytic anemia and partial deficiency of protein 4.2."; Blood 80:523-529(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-92329950; PubMed-1378323;
Jarolim P., Palek J., Rubin H.L., Prchal J.T., Korsgren C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION OF TYR-8; TYR-21; TYR-359 AND TYR-904
MEDLINE-20400020; Pubmed-10942405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 88:11022-11026(1991)
                                                                                                                                                                                          665-688.
                                                                                                                                                                                        ROLE OF GLU-681, AND SEQUENCE OF (
MEDLINE-92332495; Pubmed-1352774;
                                                                                                                                                                                                                                                                                                                         MEDLINE-91358422; PubMed-1885574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT HE 400-ALA--ALA-408 DEL. MEDLINE-92167271; PubMed-1538405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . Mol. Biol. 223:949-958(1992),
                                      Biochem. J. 213:577-586(1983).
                                                                                                                                                                                                                                                                                                        PALMITOYLATION OF CYS-843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT MEMPHIS GLU-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT HS ARG-327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nash G.B., Dlu
Gratzer W.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Basis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cohen C.1
```

```
Bruce L.J., Kay M.M., Lawrence C., Tanner M.J.; "Band 3 HT, a human red-cell variant associated with acanthocytosis and increased anion transport, carries the mutation Pro-868-->Leu in the membrane domain of band 3."; Biochem. J. 293:317-320(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alloisio N., Texier P., Vallier A., Ribeiro M.L., Morle L., Bozo
Bursaux E., Maillet P., Goncalves P., Tanner M.J., Tamagnini G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANTS HS GLN-760; TRP-760; CYS-808 AND TRP-870.
MEDLINE=95134893; PubMed=7530501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT BLOOD GROUP DI(A)/MEMPHIS-II. MEDLINE-94266802; PubMed-8206915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transmembrane segment 11.";
Br. J. Haematol, 91:804-810(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANTS HS SER-147 AND MET-488.
MEDLINE-97351102; PubMed-9207478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conditions.";
Blood 85:541-547(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fanner M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [23]
VARIANTS HS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Palek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19
      RRT REPARENTED BY SERVICE SERV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brunati A.M., Bordin L., Clari G., James P., Quadroni M., Baritono E., Pinna L.A., Donella-Deana A.; "Sequential phosphorylation of protein band 3 by Syk and Lyn tyrosine kinases in intact human erythrocytes: identification of primary and secondary phosphorylation sites."; Blood 96:1550-1557(2000).
                                                                                                                                                                                         ï.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-91329825; PubMed-1678289; Yannoukakos D., Vasseur C., Driancourt C., Blouquit Y., Delauney J., Walcman H., Bursaux E.; Blouman Erythrocyte band 3 polymorphism (band 3 Memphis): characterization of the structural modification (Lys 56-->Glu) by protein chemistry methods."; Blood 78:1117-1120(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tuscaloosa: Pro-327-->Arg substitution in the cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unique red cell membrane properties in hereditary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-93343855; PubMed-8343110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /ARIANT HS LEU-868
```

Jarolim P., Rubin H.L., Brabec V., Chrobak L., Zolotarev A.S., Alper S.L., Brugnara C., Wichterle H., Palek J.; "Mutations of conserved arginines in the membrane domain of erythroid band 3 lead to a decrease in membrane-associated band 3 and to the phenotype of hereditary spherocytosis."; Blood 85:634-640(1995). "Human erythrocyte protein 4.2 deficiency associated with hemolytic anemia and a homozygous 40 glutamic acid-->lysine substitution in the cytoplasmic domain of band 3 (band 3Montefiore)."; Eluce L.J., Anstee D.J., Spring F.A., Tanner M.J.;
"Band 3 Memphis variant II. Altered stilbene disulfonate binding and
the Diego (Dia) blood group antigen are associated with the human
erythrocyte band 3 mutation Pro-884-->Leu.";
J. Biol. Chem. 269:16155-16158(1994). Bozon M., VARIANT HS ASP-771.
MEDLINE-96136073; PubMed=8547122;
Maillet P., Vallier A., Reinhart W.H., Wyss E.J., Ott P., Texier P.,
Baklouti F., Tanner M.J., Delaunay J., Alloisio N.;
"Band 3 Chur: a variant associated with band 3-deficient hereditary
spherocytosis and substitution in a highly conserved position of d with a site of VARIANTS HS LYS-40; CYS-518 AND MET-663 DEL.
MEDLINE-96225450; PubMed-8640229;
Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,
Dornwell M., Herbers J., Kuujer W., Oezcan R., Pekrun A.,
Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;
"Ankyzin-1 mutations are a major cause of dominant and recessive hereditary spherocytosis.";
Nat. Genet. 13:214-218(1996). "Changes in the blood group Wright antigens are associated with mutation at amino acid 658 in human erythrocyte band 3: a site cinteraction between band 3 and glycophorin A under certain "Characterization of 13 novel band 3 gene defects in hereditary spherocytosis with band 3 deficiency."; Blood 88:4366-4374(1996). MEDLINE-97099297; PubMed-8943874; Jarolim P., Murray J.L., Rubin H.L., Taylor W.M., Prchal J.T., Ballas S.K., Snyder L.M., Chrobak L., Melrose W.D., Brabec V., VARIANT MONTEFIORE LYS-40.
MEDLINE-93229758; PubMed-8471774;
Rybicki A.C., Qiu J.J.H., Musto S., Rosen N.L., Nagel R.L., Schwartz R.S.; VARIANT BLOOD GROUP WR(A). MEDLINE-95111140; PubMed-7812009; Bruce L.J., Ring S.M., Anstee D.J., Reid M.E., Wilkinson S. VARIANTS HS ASP-285; GLU-455; PRO-707; PRO-834 AND MET-837

 \sim

```
RESULT 3
ŏ
                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ibb.ch).
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. IN THE BASOLATERAL MEMBRANE OF INTERCALATED CELLS OF DISTAL TUBULES AND
                                                                                                                                                                                                                                                       01-NOV-1991 (Rel. 20, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Band 3 anion transport protein (Anion exchange protein 1) (AE 1).
SLC4Al OR AEI.
                           .;
0
         Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00219; ANION EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;
                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: Kidney.
SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Event-Alternative splicing; Named isoforms-2;
      100.0%; Score 112; DB 1;
100.0%; Pred. No. 3.2e-09;
ive 0; Mismatches 0;
                                                                                                                 927 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Kidney;
IsoId=P23562-2; Sequence=VSP_000455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId-P23562-1; Sequence-Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P02730, IBTS.
InterPro: IPR001717; Anion_exchange.
InterPro: IPR001010; HC03_cotranspt.
Pfam; PF00955; HC03_cotranspt.
PRINTS; PR01231; HC03TRNSPORT.
                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; J04793; AAA40800.1; ALT_INIT.
EMBL; L02943; AAA40801.1; -.
                                                         DRILLEKPPKYHPDVPYVK 826
                                                                                                                                                                                                                                           TISSUE-Kidney;
MEDLINE-89255254; PubMed-2722777;
                                            1 DRILLLFKPPKYHPDVPYVK 20
                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                SEQUENCE OF 46-927 FROM N.A.
                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-45 FROM N.A.
     Ouery Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FIGRFAMS; TIGRO0834; ae;
                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name-Erythrocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                       COLLECTING DUCTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A33810.
                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A33810;
                                                                                                                B3AT_RAT
P23562;
                                                                807
                                                                                            RESULT 2
                                                                                                                  á
                                                               셤
```

```
SEQUENCE FROM N.A. MEDINE-82568011; PubMed-2410791; MEDLINE-82568011; PubMed-2410791; Foption R., Lodish H.F.; Primary structure and transmembrane orientation of the murine anion exchange protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Sukaryota: Metazoa, Chordata, Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Band 3 anion transport protein (Anion exchange protein 1) (AE 1)
                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . ) (PROBABLE).
PALMITATE (BY SIMILARITY).
Missing (in isoform Kidney).
                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                             Length 927;
                                                                                                                                                                                                                                                                                                                                                                               Score 108; DB 1; Lengu...
No. 1.3e-08; Indels
                                                                                                                                   EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                                                                                                    EXOPLASMIC LOOP (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-87250387; PubMed-3036795;
Kopito R.R., Andersson M., Lodish H.F.;
"Structure and organization of the murine band 3 gene.";
J. Biol. Chem. 262:8035-8040(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUL-1987) to the EMBL/GenBank/DDBJ databases
              CYTOPLASMIC (POTENTIAL). MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                        /FTId=VSP_000455,
681A228474E5E9DE CRC64;
                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
SEQUENCE FROM N.A.
MEDLINE-86034211; PubMed-3840489;
MEDLINE - 86034211; PubMed-3840489;
"Structure of the murine anion exchange protein.";
"Structure of the murine anion exchange protein.";
"Structure of the murine anion exchange protein.";
 splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     929 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                 POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                      POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                        POTENTIAL. POTENTIAL.
                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [5]
SEQUENCE OF 11-929 FROM N.A.
MEDLINE-86274622; PubMed-3015590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DRILLERPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                           103172 MW;
                                                                                                                                                                                                                                                                                                                                                                                                             96.4%;
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exchange protein.";
Nature 316:234-238(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
Palmitate
                                                                                                                                                                                                    676
696
696
735
735
882
882
883
859
859
                                                                                                                                                                                                                                                                                                                                                                         927 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Kopito R.R.;
                                                                                                                 540
559
585
605
641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MEBS).
SLC4Al OR AEl.
 Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B3AT_MOUSE
P04919;
                              DOMAIN
TRANSMEM
TRANSMEM
                                                                               TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                        TRANSMEM
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  823
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                      TRANSMEM
                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                         VARSPLIC
                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                    DOMAIN
                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B3AT_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MEB3
```

. O

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                          "Major proteolytic fragments of the murine band 3 protein as obtained after in situ proteolysis.";
Blochim. Biophys. Acts 980:291-298(1989).
FUNCTION: BAND 3 IS THE MAJOR INTEGRAL GLYCOPROTEIN OF THE EXTTHROCYTE MEMBRANE. BAND 3 HAS TWO FUNCTIONAL DOMAINS. ITS INTEGRAL DOMAIN MEDIATES A 1.1 EXCHANGE OF INORGANGIC ANIONS ACROSS THE MEMBRANE, WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING SITES FOR CYTOSKELETAL PROTEINS, GLYCOLYTIC ENZYMES, AND
                                                                                                                                                                                                                                                                                                            SUBGNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY SUBCELLULARS TO BE TETRAMERIC.
SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS:
Demuth D.R., Showe L.C., Ballantine M., Palumbo A., Fraser P.J., Cloe L., Rovera G., Curtis P.J.;
"Cloning and structural characterization of a human non-erythroid
                                                                                                                                  Raida M., Wendel J., Kojro E., Fahrenholz F., Fasold H., Legrum B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
POTENTIAL.
N-LINKED (GLCNAC. . .) (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00219; ANION EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXOPLASMIC LOOP (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
POTENTIAL.
EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                            ISOId-P04919-2; Sequence-VSP_000454;
-1- TISSUE SPECIFICITY: ERYTHROCYTE.
-1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (PÓTENTIAL).
MEMBRANE (ANION EXCHANGE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=2;
                                                                                                SEQUENCE OF 33-47; 360-375; 382-395 AND 578-590.
MEDLINE-89229233; PubMed-2713407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Palmitate; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=P04919-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X02677; CAA26506.1; --
EMBL; M29379; AAA37187.1; --
EMBL; J02756; AAA37278.1; --
EMBL; X03917; CAA27555.1; --
PIR; A25314; A25314.
HSSP; P02730; 1BTS.
MGD; MGI:109399; Slc4a1.
INTERPRO: IPRROU1717; Anion_exchange.
INTERPRO: IPRRO1717; Anion_exchange.
INTERPRO: IPRRO3020; HCO3_cotranspt.
PFAm; PF00955; HCO3_cotranspt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR01231; HCO3TRNSPORT.
                                                    band 3-like protein.";
EMBO J. 5:1205-1214(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIGRFAMS; TIGRO0834; ae;
                                                                                                                                                                                                                                                                                                                                                                                                Name-Erythrocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Kidney;
                                                                                                                                                                                                                                                                                                HEMOGLOBIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lipoprotein;
DOMAIN
                                                                                                                                                  Passow H.;
"Major prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                    9
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions along as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                        -1- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY AND APPEARS TO BE TETRAMERIC.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- TISSUE SPECIFICITY: ERYTHROCYTE.
-1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                     Gaps
                                                                                                    ö
                                                                         Length 929;
                                                            Score 108; DB 1; Lengtn >2.
Pred. No. 1.3e-08;
             79 Missing (in isoform Kidney).
/FIGAVSP_000454.
67 G -> S (IN REF. 5).
103135 MW; 5C0E281C394FB614 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane; Glycoprotein; Anion exchange; Erythrocyte.

DOMAIN 1 416 CYTOPLASMIC (POTENTIAL)

DOMAIN 417 922 MEMBRANE (ANION EXCHANGE).
 PALMITATE (BY SIMILARITY)
                                                                                                                                                                                                                                     01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
                                                                                                                                                                                                                 922 AA
                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
                                                                                                                                                                                                                PRT;
                                                                                                                                       1 DRILLLFKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00955; HC03 cotransp; 1.
PRINTS; PR01231; HC03TRNSPORT.
TIGREAMS; TIGREAMS; ae; 1.
                                                                                                                                                                                                                                                                            Band 3 anion transport protein. Gallus gallus (Chicken).
                                                                         96.4%;
95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M23404; AAA48753.1; -. HSSP; P02730; 1BTQ.
                                                                                     1 Similarity 95.0 19; Conservative
                                                                                                                                                                                                                 STANDARD;
                                    467
929 AA;
                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
                                                                                                                                                                                                                B3AT_CHICK
P15575;
LIPID
VARSPLIC
                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
TRANSMEM
TRANSMEM
                                   CONFLICT
                                               SEQUENCE
                                                                                     Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRANSMEM
                                                                                                                                                                                                                                                                                                                               Gallus
                                                                                                 Matches
 SFFF
                                                                                                                          ò
                                                                                                                                                Q
```

3 19:34:06 2003

ded Sep

```
5.1.6
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2003
```

protein search, using sw model protein ŏ 3; Search time 17.25 Seconds (without alignments)
111.500 Million cell updates/sec 3, 2003, 11:41:03 September Run on:

US-10-087-464-1

1 GMPWLSATTVRSVTHANALT 20 score: Perfect so Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues hed:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	band 3 anion trans	band 3 anion trans	band 3 protein - m	anion transporter	band 3 anion trans	band 3 anion trans	band 3 anion trans	band 3 protein, no	band 3-related pro	band 3-related pro	3-related		anion exchanger 3,	band 3-related pro	erythrocyte anion	anion exchanger 3	band 3 anion trans	hypothetical prote	probable lipoic ac	sodium bicarbonate	sodium bicarbonate	sodium bicarbonate	Na+ bicarbonate co	sodium bicarbonate	hypothetical prote	hypothetical prote	cobalamin biosynth		probable sodium bi
SUMMAKIES	OI .	A33810	взни	A25314	I50159	A30816	S59861	S24318	A25104	A34911	A31789	A56764	S21086	A42497	B34911	A33638	I38496	S31828	T28858	T44895	T31336	T13962	T14110	PC7034	T14031	C72506	B72722	F69000	A56879	T37460
	DB	7	Н	7	Ġ	7	~	7	7	7	~	7	~	~	∾.	~	N	N	~	~	~	7	~	~	7	7	7	7	7	~
	Query Match Length	848	911	929	844	922	912	918	865	1234	1237	1237	1240	1030	1227	1227	1232	357	826	314	1035	1035	1035	1079	1079	156	111	302	727	1119
ď	Query Match	100.0	100.0	100.0	96.2	96.2	91.3	91.3	89.4	89.4	89.4	89.4	89.4	85.6	85.6	85.6	85.6			46.2	45.2	45.2	45.2	45.2	45.2	44.2	43.3	43.3	43.3	43.3
	Score	104	104	104	100	100	95	95	93	93	93	93	93	89	88	88	88	84	53	48	47	47	47	47	47	46	45	45	45	45
	Result No.	1	2	3	4	2	9	7	80	6	10	11	. 12	13	14	15	16	17	18	19	20	21	22	23		25		. 27	28	29

hypothetical prote probable cytochrom hypothetical prote	hypothetical prote NADH2 dehydrogenas	hypothetical prote probable lipoic ac	hypothetical prote PHO85-like protein	u-plasminogen acti cytochrome c-type hypothetical prote	cytochrome c-type iron binding prote	hypothetical prote glycine betaine/L-
T22491 H70526 T27828	T27829 T11840	D83699 C70787	T22841 T42379	UNHU E57987 D86101	H91260 T45065	D83563 MMECPW
999	100	0,010	707	7 7 7	77	7 7
1175	1519	305	415	552 552 552	552 332	354
m, m, m		m m c	ى ش د	20.0	0.4	4.4
444	4 4 4	44.	4 4	4 4 4	4 4	4 4
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	44	4 4 8	444	42.5 42.5	42.5	4 4 2 2
30	. e. e.	w.w. w.w.	38	4 4 4 1 4 1 4 1 4 1 4 1 4 1 4 1 4 1 4 1	4 4 3 8	44 45

ALIGNMENTS

transport protein - rat band 3 anion

C;Species: Rattus norvegicus (Norway rat) C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 20-Aug-1999 C;Accession: A33810

E;Kudrycki, K.E.; Shull, G.E. J. Biol. Chem. 264, 8185-8192, 1989 A;Title: Primary structure of the rat kidney band 3 anion exchange protein deduced fr A;Reference number: A33810; MUID:89255254; PMID:2722777 A;Accession: A33810

A Status: preliminary A Molecule type: mRNA A; Residues: 1-848 < KUD>

A; Cross-references: GB:J04793; NID:g203092; PIDN:AAA40800.1; PID:g203093 C; Superfamily: band 3 anion transport protein C; Keywords: alternative splicing; transmembrane protein

Gaps ; 0 Length.848; Indels Score 104; DB 2; Pred. No. 8.3e-09; 100.0%; 100.0%; Query Match Best Local Similarity Matches 20; Conserv

ö

Mismatches 1 GMPWLSATTVRSVTHANALT 20 ö Conservative ò

GMPWLSATTVRSVTHANALT 676 q

RESULT 2

band 3 anion transport protein, erythrocyte - human N; Alternate names: carrier family 4, anion exchanger, member 1; erythroid anion excha C; Species: Homo sapiens (man) C; Date: 03-Aug-1984 #sequence_revision 03-Oct-1995 #text_change 22-Jun-1999 C; Accession: A36218; S03074; I39408; I39409; A92237; A26507; A92430; A90323; A28079; R; Lux, S.E.; John, K.M.; Kopito, R.R.; Lodish, H.F. Proc. Natl. Acad. Sci. U.S.A. 86, 9089-9033, 1989 A;Ttle: Cloning and characterization of band 3, the human erythrocyte anion-exchange A; Reference number: A36218; MUID:90083213; PMID:2594752

A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-911 <LUX>

A; Cross-references: GB:M27819; NID:g178215; PIDN:AAA35514.1; PID:g178216
R; Tanner, M.J.A.; Martin, P.G.; High, S.
Blochem, J. 256, 703-712, 1988
A; Title: The complete anino acid sequence of the human erythrocyte membrane anion-tra
A; Reference number: S03074; MUID:89134172; PMID:3223947

A;Molecule type: mRNA A;Residues: 1-55,/E°,75-911 <TAN> A;Cross-references: EMBL:X12609; NID:928713; PIDN:CAA31128.1; PID:928714 R;Showe, L.C.; Ballantine, M.; Huebner, K.

ပ္ပ

```
A25314

Dand 3 protein - mouse

C; Species: Max musculus (house mouse)

C; Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 20-Aug-1999

C; Accession: A25314; A26086; I49524; B25104

E; Kopito, R. R.; Lodish, H.F.

Nature 316, 234-238, 1985

A; Title: Primary structure and transmembrane orientation of the murine anion exchange
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Note: sequence extracted from NCBI backbone (NCBIP:113819, NCBIP:11381, NCBIP:1138 A;Note: a histidine residue essential for anion transport is suggested to be His-651, R;Okubo, R; Kang, D.; Hamssaki, N.; Jennings, M.L.
3. Biol. Chem. 269, 1918-1926, 1994
A;Title: Red blood cell band 3. Lysine 539 and lysine 851 react with the same H-2DIDS A;Reference number: A49717; MUID:94124538; PMID:8294441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Molecule type: protein
A;Rosidues: 427-436;479-519;538-540;559-566;809-817;825-841;849-857 < CKU>
A;Rosidues: 427-436;479-519;538-540;559-566;809-817;825-841;849-857 < CKU>
A;Note: Lys-539 and Lys-851 were shown to bind the same molecule of the anion transpo R;Hamasaki, N.; Okubo, K.; Kuma, H.; Kang, D.; Yae, Y.
J. Biochem. 122, 577-585, 1997
A;Title: Proteolytic cleavage sites of band 3 protein in alkali-treated membranes: Fi
A;Reference number: PC4403; MUID:98006310; PMID:9348087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Keywords: acetylated amino end; glycoprotein; ion transport; phosphoprotein; transm 1-403/Region: cytoskeletal protein binding 404-911/Region: anion antiporter
                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 361-372;390-399;604-613;632-639;647-656;699-729;731-743;761-781;818-826
A; Experimental source: erythrocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Comment: Band 3 is the major integral glycoprotein of the erythrocyte membrane. A C;Comment: Band 3 has at least two functional domains. Its integral domain mediates ing sites for cytoskeletal proteins, glycolytic enzymes, and hemoglobin.
R;Kang, D.; Okubo, K.; Hamasaki, N.; Kuroda, N.; Shiraki, H.
J. Balol. Chem. 267, 19211-19217, 1992
A;Title: A structural study of the membrane domain of band 3 by tryptic digestion.
A;Reference number: A44116; MUID:92406862; PMID:1527044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;642/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1/Modified site: acetylated amino end (Met) #status experimental 539,590,851/Binding site: anion (Lys) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transmembrane #status predicted <TM05>
transmembrane #status predicted <TM06>
transmembrane #status predicted <TM07>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transmembrane #status predicted <TMO8>
transmembrane #status predicted <TMO9>
transmembrane #status predicted <TMIO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transmembrane #status predicted <TM11>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *861-881/Domain: transmembrane #status predicted <TM14>*I/Modified site: acetylated amino end (Met) #status ex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            predicted <TMO4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transmembrane #status predicted <TM12>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transmembrane #status predicted <TM13>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            predicted predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transmembrane #status predicted
transmembrane #status predicted
transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 104;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Map position: 17q21-17q22 Superfamily: band 3 anion transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: GDB:119874; OMIM:109270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
llarity 100.0%;
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GMPWLSATTVRSVTHANALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein A; Residues: 361-911 <HAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: GDB: SLC4A1; EPB3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 20; Conserv
                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                405-427/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -780/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .-507/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  604-624/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -806/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -457/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -542/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -680/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -721/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -479/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -588/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     839-859/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 559 630 <BRO>
A; Note: Lys-590 was shown to bind phenyl isothiccyanate, an inhibitor of anion transport
A; Note: Lys-500 was shown to bind phenyl isothiccyanate, an inhibitor of anion transport
B; Rawano, Y; Okubo, K; Tokunaga, F; Miyata, T; Iwanaga, S.; Hamasaki, N.
J. Biol. Chem. 263, 8232-8238, 1988
A; Title: Localization of the pyridoxal phosphate binding site at the COOH-terminal regic
A; Reference number: A28079; MUID:88228050; PMID:3372523
                           A; Title: Localization of the gene for the erythroid anion exchange protein, band 3 (EMPE A; Reference number: 139408; MUID:88031311; PMID:3478298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R.Drickamer, L.K.

B.Do. Chem. 253, 7242-7248, 1978

A;Title: Orientation of the band 3 polypeptide from human erythrocyte membranes. Identif
A;Reference number: A92237; MUID:79027186; PMID:701248

A;Recession: A92237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecule type: protein Residues: 1-3 CDRIX MUD: Residues: 1-3 CDRIX MUJ: Findlay, J.B.C. Cohem. J. 205, 465-475, 1982 Action and partial sequence of di-lodosulphophenyl isothiocyanate-bin Reference number: A26507; MUD: 83074521; PMID:7150226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Human erythrocyte band 3 polymorphism (band 3 Memphis): characterization of the A; Reference number: A44933; MUD:91329825; PMID:1678289
A; Accession: A44933
A; Accessi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 1-201;220-292;307-308, 'R',310-312,'S',314-329,'K',331-333;347-370 < YANI>
R; Cobb, C.E.; Beth, A.H.
Biochemistry 29, 8283-8290, 1990
A; Title: Identification of the eosinyl-5-maleimide reaction site on the human erythrocyt
A; Reference number: A35835; MUID:91070049; PMID:1701324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human erythrocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Molecule type: protein
Residues: 834-842, 7X', 844-911 cKAW>
Residues: 834-842, 7X', 844-911 cKAW>
Residues: 834-842, 7X', 844-911 cKAW>
Residues: Rid-Residues: 834-842, 7X', 844-911 cKAW>
Residues: Rid-Residues: Rid-Residue Rid-Res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Realduse: 37-56 <SHO1>
A;Cross-references: GB:M16978; NID:g178217; PIDN:AAA51670.1; PID:g178220
A;Accession: 139409
                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 118-161 <SHO2>
A;Cross-references: GB:M16979; NID:9178218; PIDN:AAA51671.1; PID:9553169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A; Residues: 437-473;360-364, 'D',366-369 < MAW>
R; Kaul, R.K.; Murthy, S.N.P.; Reddy, A.G.; Steck, T.L.; Kohler, H.
J. Biol. Chem. 258; 7981-7990, 1983
A; Title: Amino acid sequence of the N(alpha)-terminal 201 residues of A; Reference number: A92430; MUD:83238395; PMID:6345535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: The human erythrocyte anion-transport protein. A; Reference number: A90323; MUID:83308584; PMID:6615451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 1-10, D; 12-68, E', 69-200 < KAU>
R; Brock, C.J.; Tanner, M.J.A.; Kempf, C.
Blochem. J. 213, 577-586, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A92430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: A28079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A26507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A90323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S05523
```

A; Reference A; Accession

```
R;Fievet, B.; Gabillat, N.; Borgese, F.; Wotais, R.
EMBO J. 14, 5158-5169, 1995
A;Title: Expression of band 3 anion exchanger induces chloride current and taurine tr
A;Reference number: S59861; MUID:96080151; PMID:7489705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cyaccession: S24318; S36083; S22173
R;Huebner, S.; Michel, F.; Rudloff, V.; Appelhans, H.
Blochem, J. 2855, 17-23, 1992
A;Ittle: Amino acid sequence of band-3 protein from rainbow trout erythrocytes derive A; reference number: S24318; MUID:92344566; PMID:1637296
                                                                                                                                                                                                                  A; Cross references: EMBL: 250848; NID:91004316; PIDN: CAA90701.1; PID:91004317 C; Superfamily: band 3 anion transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           band 3 anion transport protein - rainbow trout
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 band 3 anion transport protein isoform b - rainbow trout
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 20-Aug-1999
                                                                                                                                                                                                       #sequence_revision 30-Sep-1991 #text_change 16-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: EMBL:X61699; NID:g64308; PIDN:CAA43868.1; PID:g64309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 100; DB 2;
Pred. No. 4.1e-08;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 95; DB 2;
Pred. No. 2.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, August 1991
A;Reference number: S22173
A;Accession: S22173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-922 <KIM>A; Cross-references: GB:M23404
C; Superfamily: band 3 anion transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Accession: 524318
A,Molecule type: mRNA
A,Residues: 1-918 (HUEL>
A,Crossion: 536083
A,Accession: 536083
A,Molecule type: protein
A,Residues: 71-89:94-114;570-588 (HUEZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ,306-918 <APP>
                                                                                                                                                                                         C;Species: Gallus gallus (chicken)
C;Date: 01-Dec-1989 #sequence_revi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96.2%;
ilarity 90.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 91.3%;
Best Local Similarity 90.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-912 <FIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Residues: 1-304,'G'
                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: S59861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: S59861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Appelhans, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
S59861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S24318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 4-707, 'X', 709-902 <RES>
A; Cross-references: GB: J02756; NID: 9192136; PIDN: AAA37278.1; PID: 9553874
R; Demuth, D. R.; Showe, L.C.; Ballantine, M.; Palumbo, A.; Fraser, P.J.; Cloe, L.; Rovera
EMBO J. 5, 1205-1214, 1986
A; Title: Cloning and structural characterization of a human non-erythroid band 3-like pr
A; Reference number: A91039; MUID: 86274622; PMID: 3015590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Introns: 5/3; 46/1; 70/3; 131/1; 176/2; 217/3; 245/1; 305/3; 376/1; 447/1; 496/3; 561/
C;Superfamily: band 3 anion transport protein
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M19496; NID:g211211; PIDN:AAA48604.1; PID:g211212
C;Superfamily: band 3 anion transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                            A Molecule type: mRNA

A. Residues: 1-929 < KRO.>

A. Residues: 1-929 < KRO.>

A. Cross-references: GB: MZ9379; NID:g191741; PIDN: AAA37187.1; PID:g191742

R. Kropito, R. R.; Andersson, M.; Lodish, H. F.

B. Brol. Chem. 262, 8035-8040, 1987

A. Hitle: Structure and organization of the murine band 3 gene.

A. Reference number: 149524; MUID:87250387; PMID:3036795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 11-466,'S',468-929 <DEM>
A;Cross-references: GB:X03917; NID:953042; PIDN:CAA27555.1; PID:953043
C;Genetics:
                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-929 < KOP>
A; Residues: 1-929 < KOP>
A; Cross-references: GB: X02677; NID:g49897; PIDN:CAA26506.1; PID:g49898
B; Kopito, R.R.; Lodish, H.F.
J. Cell. Blochem. 29, 1-17, 1985
A; Title: Structure of the murine anion exchange protein.
A; Reference number: A26086; MUID:86034211; PMID:3840489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels

    chicken

                                                                                                                                                                                              number: A25314; MUID:85268011; PMID:2410791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 104; DB 2;
Pred. No. 9.2e-09;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 100; DB 2;
Pred. No. 3.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A30816
band 3 anion transport protein (clone pBIIIC1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GMPWLSATTVRSVTHANALT 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.2%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%;
Matches 20; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-844 <COX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: I49524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: B25104
                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A26086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

ô

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

protein search, using sw model OM protein 3; Search time 17.25 Seconds (without alignments) 111.500 Million cell updates/sec 3, 2003, 11:41:03 September Run on:

US-10-087-464-2 98 Title: Perfect score:

1 SVTHANALTVMGKASTPGAA 20 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

283308 number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 0B 0B Minimum Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_76:*
1: pir1:*
3: pir2:*
: pir3:*
: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

polyketide synthas hypothetical prote	orfl 5' to fcc - S	triosephosphate is	triosephosphate is	geranylgeranyl dip	ABC transporter, s	probable solute-bi	probable nucleic a	probable RTX famil	hypothetical prote	latent transformin	translation initia	hypothetical prote	hypothetical prote	methionine aminope
T17409	A44238	AH2775	F97555	C75400	AG2724	C97506	H75272	B85547	F90696	A55494	AE3544	A82459	T37094	B87106
77	٠,	7	7	7	~	ď	7	C)	~	7	~	7	7	C4 .
4613	122	256	256	329	497	509	603	5188	5291	1820	128	144	206	285
42.9	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.3	40.8	40.8	40.8	40.8
42	41.7	41	41	41	41	41	41	41	41	40.5	40	40	40	40

ALIGNMENTS

Danig a anion transport protein, erythrocyte - human N;Alternate names: carrier family 4, anion exchanger, member 1; erythroid anion exchanger, statemate names: carrier family 4, anion exchanger, member 1; erythroid anion exchange c) Species: Home Sapiens (man) (c) Accession 3-Oct-1995 #text_change 22-Jun-1999 (c) Accession: A36218; S03074; I39408; I39409; A92237; A26507; A92430; A90323; A28079; R;Lux, S.E.; John, K.M.; Kopito, R.R.; Lodish, H.F. Proc. Natl. Acad. Sci. U.S.A. 86, 9089-9093, 1989 A;Feference number: A36218; MuID:90083213; PMID:2594752 A;Accession: A36218

A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-91 cLUX>
A;Cross-references: GB:M27819; NID:g178215; PIDN:AAA35514.1; PID:g178216
B;Tanner, M.J.A.; Martin, P.G.; High, S.
Biochem J. 256, 703-712, 1988
A;Title: The complete amino acid sequence of the human erythrocyte membrane anion-tr
A;Reference number: S03074; MUID:89134172; PMID:3223947

A; Molecule type: mRNA A; Residues: 1-55, E', 57-911 <TAN> A; Cross-references: EMBL:X12609; NID:g28713; PIDN:CAA31128.1; PID:g28714 A; Cross-references: EMBL:X12609; NID:g28713; PIDN:CAA31128.1; PID:g28714 R; Showe, L.C.; Ballantine, M.; Huebner, K. Genomics 1, 71-76, 1987 A; Title: Localization of the gene for the erythroid anion exchange protein, band 3 (A; Reference number: 139408; MUID:88031311; PMID:3478298 A;Molecule type: DNA A;Residues: 37-56 cSHO1> A;Cross-references: GB:M16978; NID:g178217; PIDN:AAA51670.1; PID:g178220 A;Accession: I39409

A;Molecule type: DNA A;Residues: 118-161 <SHO2> A;Cross-references: GB:M16979; NID:g178218; PIDN:AAA51671.1; PID:9553169

R;Drickamer, L.K. J. Biol. Chem. 253, 7242-7248, 1978 A;Title: Orientation of the band 3 polypeptide from human erythrocyte membranes. Ide A;Reference number: A92237; MUID:79027186; PMID:701248

A; Molecule type: protein A; Residues: 1-3 <DRI> R; Mawby, W. J.; Findlay, J.B.C. Biochem. J. 205, 465-475, 1982 A; Title: Characterization and partial sequence of di-iodosulphophenyl isothiocyanate A; Reference number: A26507; MUID:83074521; PMID:7150226

A;Molecule type: protein A;Residues: 437.473;360-364,'D',366-369 <MAW> R;Kaul, R.K.; Murthy, S.N.P.; Reddy, A.G.; Steck, T.L.; Kohler, J. Biol. Chem. 258, 7981-7990, 1983

Ξ

ø

integral domain mediates

Its

```
A33810
band 3 anion transport protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 20-Aug-1999
                                                                                         enzymes, and hemoglobin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.Cross-references: GB:J04793; NID:g203092; PIDN:AAA40800.1; PID:g203093; C:Superfamily: band 3 anion transport protein C:Keywords: alternative splicing; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F:642/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Met) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F:1/Modified site: acetylated amino end (Met) #status experi
F:539,590,851/Binding site: anion (Lys) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <TM11>
<TM12>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;839-859/Domain: transmembrane #status predicted <TM13>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F:861-881/Domain: transmembrane #status predicted <TM14>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 91; D. .,
Pred. No. 6.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;764-780/Domain: transmembrane #status predicted F;78-806/Domain: transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.9%; Score 91; DB 2; 95.0%; Pred. No. 6.7e-07
                                         Comment: Band 3 has at least two functional do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 98;
                                                                                                                                                                   GDB:119874; OMIM:109270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SVTHANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SVTHANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
les 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 92.98
Best Local Similarity 95.08
Matches 19, Conservative
                                                                                                                                   A; Gene: GDB:SLC4A1; EPB3
                                                                                                                                                                A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                         C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                       A.Molecule type: protein
A.Residues: 559-630 <BRO>
A.Note: Lys-590 was shown to bind phenyl isothiocyanate, an inhibitor of anion transport
A.Note: Lys-590 was shown to bind phenyl isothiocyanate, an inhibitor of anion transport
B.Note: Lys-590 was shown to bind phenyl isothiocyanate, an inhibitor of anion transport
J. Biol. Cham. 263, 8332-838, 1988
A.Title: Localization of the pyridoxal phosphate binding site at the COOH-terminal regic
A.Reference number: A28079; MUID:88228050; PMID:3372523
A;Title: Amino acid sequence of the N(alpha)-terminal 201 residues of human erythrocyte A;Reference number: A92430; MUD:83238395; PMID:6345535
A;Accession: A92430
A;Accession: A92430
A;Residues: 1-10, 'D',12-68,'E',69-200 < KAU>
B;Brock, C.J; Tanner, M.J.A; Kempf, C.
Biochem: J. 213, 577-586, 1983
A;Title: The human erythrocyte anion transport protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Wolecule type: protein
A; Molecule type: protein
A; Residues: 1-55, E',57-69 <YAN2>
A; Note: sequence extracted from NCBI backbone (NCBIP:49829)
A; Note: sequence of a common polymorphic form designated band 3 Memphis
B; Mote: sequence of a common polymorphic form designated band 3 Memphis
B; Mote: sequence of a common polymorphic form designated band 3 Memphis
B; Mote: sequence of a common polymorphic form designated band 3 Memphis
A; Mote: sequence from NCBI backbone (NCBIP:49829)
A; Mote: sequence from NCBIP:49829
A; Mote: sequence from NCBIP:498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blood 78, 1117-1120, 1991
A:Title: Human erythrocyte band 3 polymorphism (band 3 Memphis): characterization of the
A:Reference number: A44933; MUID:91329825; PMID:1678289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Accession: A28079
A. Culle type: protein
A. Culle type: protein
A. Culle type: protein
A.Accession: Assession: Assession: S05523; MuID:90001294; PMID:2790053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Delaunay, J.; Wajcman, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBIP:113821, NCBIP:113823,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Notecle 179: protein
A;Robleule 179: 177-436;479-519;538-540;559-566;809-817;825-841;849-857 < CKU>
A;Rosidues: 427-436;479-519;538-540;559-566;809-817;825-841;849-857 < CKU>
A;Note: Lys-539 and Lys-851 were shown to bind the same molecule of the anion transport R;Hamasaki, N.; Okubo, K.; Kuma, H.; Kang, D.; Yae, Y.
T Riochem. 122, 577-585, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ldues: 361-911 <HAM>
Ment: Band 3 is the major integral glycoprotein of the erythrocyte membrane. A dime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Wolecule Type: protein
A; Residues: 361-372;390-399;604-613;632-639;647-656;699-729;731-743;761-781;818-826 <Ki.
A; Residues: 361-372;390-399;604-613;632-639;647-656;699-729;731-743;761-781;818-826 <Ki.
A; Residues: erythrocyte
A; Note: a distidine residue essential for anion transport is suggested to be His-651; 18; Note: a histidine residue essential for anion transport is suggested to be His-651; 13.
Biol. Chem. 269, 1918-1925, 1994
A;Title: Red blood cell band 3. Lysine 539 and lysine 851 react with the same H-2DIDS A; Reference number: A49717; MUID:94124538; PMID:8234441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     erythrocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule, type: protein
A; Residues: 361-364, 'X', 366-372;424-429, 'X', 431-434 <COB>
A; Note: Lys-430 is labeled by eosinyl-5-maleimide (EMA) in intact
R; Yannoukakos, D; Vasseur, C.; Driancourt, C.; Blouquit, Y.; Dela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary
```

.. 0

Gaps

; 0

anion exchange Dand 3 protein - mouse C; Species: Mus musculus (house mouse) C;Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 20-Aug-1999 C;Accession: A25314; A26086; I49524; B25104 B.Kopito, R.R.; Lodish, H.F. Nature 316, 234-238, 1985 A;Title: Primary structure and transmembrane orientation of the murine anion

ö

A;Reference number: A25314; MUID:85268011; PMID:2410791 A;Accession: A25314

Status: preliminary; translated from GB/EMBL/DDBJ

ĭ

```
conceptua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RiLindsey, A.E.; Schneider, K.; Simmons, D.M.; Baron, R.; Lee, B.S.; Kopito, R.R. Proc. Natl. Acad. Sci. U.S.A. 87, 5278-5282, 1990.
Aftitle: Functional expression and subcellular localization of an anion exchanger A; Reference number: A35770; MUID:90319095; PMID:2371270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           band 3-related protein - mouse
(;Species: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 20-Aug-1999
C;Accession: A31789
R;Alper, S.L.; Kopito, R.R.; Libresco, S.M.; Lodish, H.F.
A; Biol. Chem. 263, 17092-17099, 1988
A;Title: Cloning and characterization of a murine band 3-related cDNA from kidney
A;Reference number: A31789; MUID:89034212; PMID:3182834
C;Species: Rattus norvegicus (Norway rat)
C;Species: Vo-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 20-Aug-1999
C;Accession: A34911; A3570
C;Accession: A34911; A3570
B;Kudrycki, K.E.; Newman, P.R.; Shull, G.E.
J. Biol. Chem. 265, 462-471, 1990
J. Biol. Chem. 265, 462-471, 1990
A;Title: CDNA cloning and tissue distribution of mRNAs for two proteins that are a A;Reference number: A34911; MUID:90094439; PMID:2294114
                                                                                                                                                                                                                                                                                                                                                                                                                                                      .1; PID:9203091
Lee, B.S.; Kopito, R.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <LIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dand 3-related protein, ileum - rabbit
C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 20-Aug-1999
C; Accession: A56764, J.W.; Aronson, P.S.; Igarashi, P.
Am. J. Physiol. 263, G345-G352, 1992
A; Title: cDNA cloning and localization of a band 3-related protein from ileum. A; Reference number: A56764; MUID:93035730; PMID:1415547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary, nucleic acid sequence not shown; not compared with A;Molecule type: mRNA A;Molecule type: mRNA A;Molecule type: mRNA A;Molecule type: not compared to the sesidues: 1-205, A', 207-924, PG', 927-1017, IV', 1020-1155, ID', 1158-1234 C;Superfamily: band 3 anion transport protein C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-127 <ALP>
A; Cross-references: GB:J04036; NID:g192132; PIDN:AAA65505.1; PID:g309114
C; Superfamily: band 3 anion transport protein
C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GB:S45791; NID:9256659; PIDN:AAB23488 1; PID:9256660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1234 < KUD>
A;Residues: 1-1234 < KUD>
A;Cross-references: GB:J05166; NID:g203090; PIDN:AAA40799.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 73; DB 2; I
Pred. No. 0.00099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 73; DB 2; 1
Pred. No. 0.00099;
0; Mismatches 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1054 SVTHANALTVMSKAVAPG 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1057 SVTHANALTVMSKAVAPG 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74.5%;
illarity 83.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 74.5%;
Best Local Similarity 83.3%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1237 <CHO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A31789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Accession: B25104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: How sapiens (man)
C;Species: Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Introns: 5/3; 46/1; 70/3; 131/1; 176/2; 217/3; 245/1; 305/3; 376/1; 447/1; 496/3; 561/
C; Superfamily: band 3 anion transport protein
C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-929 < KO2>
A; Cross-references: GB:M29379; NID:g191741; PIDN:AAA37187.1; PID:g191742
A; Cross-references: GB:M29379; NID:g191741; PIDN:AAA37187.1; PID:g191742
B; Kopito, R. R.; Andersson, M.; Lodish, H.F.
J. Biol. Chem. 262, 8035-8040, 1987
A; Title: Structure and organization of the murine band 3 gene.
A; Reference number: 149524; MUID:87250387; PMID:3036795
                                                                   A; Molecule type: mRNA
A; Residues: 1-929 <ROP>
A; Cross-references: GB: CAD157; NID:g49897; PIDN:CAA26506.1; PID:g49898
A; Kopito, R.R.; Lodish, H.F.
J. Cell. Biochem. 29, 1-17, 1985
A; Title: Structure of the murine anion exchange protein.
A; Reference number: A26086; MUID:86034211; PMID:3840489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 11-466,'S',468-929 <DEM>
A;Cross-references: GB:X03917; NID:953042; PIDN:CAA27555.1; PID:953043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-865 <DEM>
A; Cross-references: GB: N30918; NID: g32120; PIDN: CAA27556.1; PID: g32121
C; Superfamily: band 3 anion transport protein
C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , DB 2; heus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 865,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 91; DB 2; Length 92>
Pred. No. 7.4e-07;
1; Indels
```

band 3 protein, nonerythroid (MEB3) - human (fragment)

1 SVTHANALIVMGKASTPGAA 20

á g

ö

Query Match 92.9%; Best Local Similarity 95.0%; Matches 19; Conservative 0

Query Match

Pred. No. 0.00); Mismatches Score 73;

ö

74.5%;

Query Match
Best Local Similarity 83.33
Matches 15; Conservative

A; Accession: A25104

SVTHANALTVMSKAVAPG 702 SVTHANALTVMGKASTPG 18

ð 셤 A34911 band 3-related protein 2

RESULT 5

OM protein - protein search, using sw model

3, 2003, 11:41:03; Search time 17.25 Seconds (without alignments) 111.500 Million cell updates/sec September ö

GKASTPGAAAQIQEVKEQRI 20 US-10-087-464-3 96 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

I number of hits satisfying chosen parameters: 283308 seqs, 96168682 residues

DB seq length: 0 DB seq length: 2000000000 ET III Maximum

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR_76:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

	Description		o anton	3 dillon C	າ	Aniton Clansporter	٦ ٣	3-related ,	יי ני	3-related	exchange c	Dand 3 and the transfer	` -	excitative	Dania 3 retained pro	erycurocyce anton	anton exchanger 3	σ		sugar - pilospilare de	adam produce de	polymerase-associa	Ω	himothetical proce		nucleobindin precu	-	hypothetical prote	hypothetical prote	Ω	
SUMMARIES	ID	ВЗНП	A33810	A25314	150159	A30816	A25104	A34911	A31789	A56764	S21086	531828	A42497	B34911	A33638	138496	T03748	F75377	DB2644	E82644	RRNZYA	RRNZED	T28858	T36321	10001	155470	2000	7700	T48429	F95386	D90938
	DB	-	~	(٠,	(7	ď	7	~	~	7	~	7	~	7	~	7	٥ ا	1 (~	-		~	c	,	۰,	۱ (V (7	~	C)
	Leng	911	848	929	844	922	865	1234	1237	1237	1240	357	1030	1227	1227	1232	1317	346	362	329	391	391	826	391	4.5	9 2 2	1360	100	1495	324	416
æ	양성	100.0	92.7	92.7		63.5		60.4	60.4	60.4	60.4	56.2	56.2			56.2			50.0	46.9	46.9	46.9	46.9		4.5. R						44.8
	Score	96	83	88	61	61	58	58	58	28	58	54	54	54	54	54	20	48	48	45	45	45		44	44		44		* •	Α.	43
	Result No.	-	7	m	4	5	9		æ	ი	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	26	200	3 6	97	67

probable transport	coronin-like prote	non-histone chromo	D-alanyl-D-alanine	hypothetical prote	probable myosin he	probable sodium bi	hypothetical prote	hypothetical prote	00] agen - nematod	acidic calmodulin-	flagellar blosynth	flagellar biosynth	probable dimethyla	protein F5M15.22 [
H85786 A64937	T38258	T38936	C97305	S60961	A71441	T37460	T22491	C84482	B44984	A46597	AI2647	H97429	H95942	B86338
77	7	7	7	~	7	~	~	~	~	~	7	~	~	7
416	601	108	241	448	527	1119	1175	159	210	220	251	251	264	265
44.8 44.8	44.8	43.8	43.8	43.8	43.8	43.8	43.8	42.7	42.7	42.7	42.7	42.7	42.7	42.7
4 4 3	43	42	42	42	42	42	42	41	41	41	41	41	41	41
30 31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Dand 3 anion transport protein, erythrocyte - human N:Alternate names: carrier family 4, anion exchanger, member 1; erythroid anion exc

Night of animon transport protein, erythrocyte - human
Night of author transport protein, erythrocyte - human
Night of author transport protein, erythrocyte - human
C. Species: Homo sapiens (man)
C. Species: Homo sapiens
C. Sacuriter family 4, anion exchanger, the constant safety and safety (species)
C. Accession: A36218, S03074, I139408; I39409; A92237; A26507; A92430; A90323; A28079.
R. Lux, S.E.; John, K.M.; Kopito, R.R.; Lodish, H.F.
Arcession: A36218
A; Reference number: A36218; MUID: 90083213; PMID: 2594752
A; Reference number: A36218; MUID: 90083213; PMID: 2594752
A; Residues: 1-91 LCLOX
A; Residues: 1-91 LCLOX
A; Residues: 1-91 LCLOX
A; Reference number: S03074; MUID: 89134172; PMID: 323947
A; Residues: 1-55, TE', 57-911 c/max
A; Reference number: S03074
A; Reference number: S03074
A; Reference number: Road Road Road Road Road Road A; Reference number: Road Bay A; Title: Localization of the gene for the erythroid anion exchange protein, band 3 (A; Reference number: 139408; MUID: 88031311; PMID: 3478298
A; Reference number: 139408; MUID: 88031311; PMID: 3478298
A; Reference number: 139408; MUID: 88031311; PMID: 3478298

A; Molecule type: DNA A; Residues: 37-56 <SHO1>

A;Cross-references: GB:M16978; NID:g178217; PIDN:AAA51670.1; PID:g178220
A;Accession: 139409
A;Accession: 139409
A;Accession: 118-161
A;Residues: 118-161 <SH02>
A;Residues: 118-161 <SH02>
A;Cross-references: GB:M16979; NID:g178218; PIDN:AAA51671.1; PID:g553169
B;Drickamer, L.K.
J. Biol. Chem. 253; 7242-7248, 1978
A;Title: Orientation of the band 3 polypeptide from human erythrocyte membranes. 1de A;Reference number: A92237; MUID:79027186; PMID:701248

A; Wolecule type: protein A; Residues: 1-3 < DRI> R; Mawby, W.J.; Findlay, J.B.C. Biochem. J. 205, 465-475, 1982 A; Title: Characterization and partial sequence of di-iodosulphophenyl isothiocyanate A; Reference number: A26507; WUID:83074521; PMID:7150226

A;Molecule type: protein A;Residues: 437-473;360-364,'D',366-369 <WAW> R;Kaul, R.K.; Murthy, S.N.P.; Reddy, A.G.; Steck, J. Biol. Chem. 258, 7981-7990, 1983

T.L.; Kohler, H.

.

ø

```
C;Species: Mus musculus (house mouse)
C;Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 20-Aug-1999
C;Dates: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 20-Aug-1999
C;Dates: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 20-Aug-1999
C;Accession: A55314, A56086, I49524; B25104
R;Kopito, R.R.; Lodish, H.F.
Nature 316, 234-238, 1985
A;Title: Primary structure and transmembrane orientation of the murine anion exchange
                                                                                                                                                                                                                                                                                                         ion transport; phosphoprotein; transm
             two functional domains. Its integral domain mediates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exchange protein deduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Residues: 1-848 < KUD>
A. Residues: 1-848 < KUD>
A. Cross-references: GB-104793; NID:g203092; PIDN:AAA40800.1; PID:g203093
C. Superfamily: band 3 anion transport protein
C. Keywords: alternative splicing; transmembrane protein
                                                sites for cytoskeletal proteins, glycolytic enzymes, and hemoglobin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 642/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Met) #status experimental #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: A33810
R;Kudrycki, K.E.; Shull, G.E.
B Blol. Chem. 264, 8185-8192, 1989
A;Title: Primary structure of the rat kidney band 3 anion A;Reference number: A33810; MUID:89255254; PMID:2722777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <TM09>
<TM10>
<TM11>
<TM12>
<TM12>
<TM13>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <TM07>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <TW08>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <TM14>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <TM04>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <TM05>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <TW06>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; L
1.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 89; DB 2; I
Pred. No. 1.2e-05;
0; Mismatches 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transmembrane #status predicted <T
                                                                                                                                                                                                        A WAD POSITION: 17421-17425
C. Superfamily: band 3 anion transport protein
C. Superfamily: band 3 anion transport protein
C. Superfamily: band 3 anion transport protein
C. Superfamily: band 3 anion transport protein; ion
C. Superfamily: band 3 anion anion
F; 1-403/Region: cytoskeletal protein binding
F; 405-427/Domain: transmembrane %status predicted
F; 435-47/Domain: transmembrane %status predicted
F; 459-47/Domain: transmembrane %status predicted
F; 522-542/Domain: transmembrane %status predicted
F; 568-588/Domain: transmembrane %status predicted
F; 568-680/Domain: transmembrane %status predicted
F; 701-721/Domain: transmembrane %status predicted
F; 701-721/D
                                                                                                                                                                                                                                                                                                                                                                                                                             transmembrane #status predicted
transmembrane #status predicted
transmembrane #status predicted
transmembrane ****
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transmembrane #status predicted transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;839-859/Domain: transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.
                                                                                                                                         EPB3
GDB:119874; OMIM:109270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /Domain: transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acetylated amino end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .590,851/Binding site: anion (Lys)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GKASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GKASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           band 3 anion transport protein - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.7%;
95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
nes 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
A25314
band 3 protein - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A33810
A; Status: preliminary
A; Molecule type: mRNA
                                                                                                                                                                             A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;1/Modified site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                      A Mesideuse type: protein
A; Mesideuse type: protein
A; Mesideuse: 559-630 caRno.
A; Title: Localization of the pyridoxal phosphate binding site at the COOH-terminal regid
A; Title: Localization of the pyridoxal phosphate binding site at the COOH-terminal regid
A; Title: Localization of the pyridoxal phosphate binding site at the COOH-terminal regid
A; Mesideuse: Massagno.
A; Resideuse: 834-842, X', 844-911 ckAN>
A; Note: Lys-851 was shown to bind the affinity label pyridoxal phosphate, a substrate for R; Yannoukakos, D: Vasseur, C: Blouquit, Y: Bursaux, E.; Wajcman, H.
Biophys. Acta 998, 43-49, 1989
A; Title: Primary structure of the cytoplasmic domain of human erythrocyte protein band 3
A; Reference number: S05523; MUID:90001294; PMID:2790053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 361-911 <HAM>
C:Comment: Band 3 is the major integral glycoprotein of the erythrocyte membrane. A dime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-201;220-292;307-308, 'R',310-312,'S',314-329,'K',331-333;347-370 < YAN1>
R; Coben (C. E.; Beth, A. H.
Blochemistry 29, 8283-8290, 1990
A; Title: Identification of the eosiny1-5-maleimide reaction site on the human erythrocyt
A; Reference number: A35835; MUID:91070049; PMID:1701324
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tryptic digestion. Confd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        < KAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: erythrocyte
A; Note: sequence extracted from NCBI backbone (NCBIP:113819, NCBIP:113821, NCBIP:113823, A; Note: sequence extracted from NCBI backbone (NCBIP:113819, NCBIP:113823, A; Note: a histidine residue essential for anion transport is suggested to be His-651, Hi R; Okubo, K.; Kang, D.; Hamasaki, N.; Jennings, M.L.
Biol. Chem. 269, 1918-1926, 1994
A; Title: Red blood cell band 3. Lysine 539 and lysine 851 react with the same H-2DIDS (4 Reference number: A49717; MUID:94124538; PMID:8294441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 427-436;479-519;538-540;559-566;809-817;825-841;849-857 <OKU>
A;Residues: 427-436;479-519;538-540;559-566;809-817;825-841;849-857 <OKU>
A;Note: Lys-539 and Lys-531 were shown to bind the same molecule of the anion transport
R;Hamasaki, N; Okubo, K.; Kuma, H.; Kang, D.; Yae, Y.
J. Biochem. 122, 577-585, 1997
A;Title: Amino acid sequence of the N(alpha)·terminal 201 residues of human erythrocyte A;Reference number: A92430; MUID:83238395; PMID:6345535 A;Accession: A92430 A;Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Proteolytic cleavage sites of band 3 protein in alkali-treated membranes: Fidel
A; Reference number: PC4403; MUID:98006310; PMID:9348087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Molecule type: protein
A; Residues: 361-364, "X', 366-372; 424-429, "X', 431-434 <COB>
A; Residues: 361-364, "X', X', 366-372; 424-429, "X', 431-434 <COB>
A; Note: Lys-430 is labeled by eosinyl-5-maleimide (EMA) in intact erythrocytes
R; Yannoukakos, D.; Vasseur, C.; Driancourt, C.; Blouquit, Y.; Delaunay, J.; Wajcman,
Blood 78, 1117-1120, 1991
Blood 78, 1117-1120, 1991
A; Ritle: Human erythrocyte band 3 polymorphism (band 3 Memphis): characterization of
A; Reference number: A44933; MUID:91329825; PMID:1678289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 361-372;390-399;604-613;632-639;647-656;699-729;731-743;761-781;818-826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A44933
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-55, Er. 57-69
A; Note: sequence extracted from NCBI backbone (NCBIP:49829)
A; Note: sequence of a common polymorphic form designated band 3 Memphis
B; D; Okubo, K; Hamasaki, N; Kuroda, N; Shiraki, H.
J; Aol. Chem. 267, 19211-19217, 1992
A; Title: A structural study of the membrane domain of band 3 by tryptic
A; Reference number: A44116; MUID:92406862; PMID:1527044
A; A44116
                                                                                                                                     A; Molecule type: protein
A; Residues: 1-10, D',12-68, E',69-200 <KAU>
R; Brochen, J. 213, 577-586, 1983
A; Title: The human erythrocyte anion-transport protein.
A; Reference number: A90323; MUID:83308584; PMID:6615451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: PC4403
A;Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A90323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: A49717
```

 \mathbf{fr}

ö

انہ ت

```
C) Accession: A30816
R) Kim, H.R.C.; Yew, N.S.; Ansorge, W.; Voss, H.; Schwager, C.; Vennstroem, B.; Zenke, R) Kim, H.R.C.; Yew, N.S.; Ansorge, W.; Voss, H.; Schwager, C.; Vennstroem, B.; Zenke, Mol. Cell. Biol. 8, 4416-4424, 1988
A) Title: Two different mRNs are transcribed from a single genomic locus encoding the A; Reference number: A30816; MUID:89039870; PMID:318555
A; Accession: A30816
A; Accession: A30816
A; Residues: 1-922 < KINS
A; Csuperfamily: band 3 anion transport protein
C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A25104

band 3 protein, nonerythroid (MEB3) - human (fragment)

band 3 protein, nonerythroid (MEB3) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999

C;Accession: A25104

R;Demuth, D.R.; Showe, L.C.; Ballantine, M.; Palumbo, A.; Fraser, P.J.; Cioe, L.; Rov

EMBO J. 5, 1205-1214, 1986

EMBO J. 5, 1205-1214, 1986

A;Title: Cloning and structural characterization of a human non-erythroid band 3-like

A;Reference number: A91039; MUID:86274622; PMID:3015590

A;Accession: A25104

A;Accession: A25104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             band 3-related protein 2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Decies: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 20-Aug-1999
C;Decession: A34911, A35770
R;KudryCki, K.E.; Newman, P.R.; Shull, G.E.
J. Biol. Chem. 265, 462-471, 1990
R;KudryCki, K.E.; Newman, P.R.; Shull, G.E.
J. Biol. Chem. 265, 462-471, 1990
R;KudryCki, K.E.; Newman, P.R.; Shull, G.E.
A;Reference number: A34911
A;Accession: A34911
A;Accession: A34911
A;Accession: A34911
A;Status: preliminary
A;Molecule type: MRNA
A;Residues: 1-1234 <a href="https://doi.org/10.100/">ktuber/abs// Aignolecule type: MRNA
A;Reference number: A35770; MulD:90319095; PMID:2371270
A;Recession: A35770
A;Recession: A3770
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1.205, "A', 207-924, 'PG', 927-1017, 'IV', 1020-1155, 'ID', 1158-1234 <LIN>C; Superfamily: band 3 anion transport protein
C:Species: Gallus gallus (chicken)
C:Date: 01-Dec_1989 #sequence_revision 30-Sep-1991 #text_change 16-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;MOJecule type: mRNA
A;Residues: 1-865 <DEM>
A;Residues: 1-865 <DEM>
A;Cross-references: GB:X03918; NID:g32120; PIDN:CAA27556.1; PID:g32121
C;Superfamily: band 3 anion transport protein
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 61; DB 2;
Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 58;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               697 KAVAPGDKPKIQEVKEQRV 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GKASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 KASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.5%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 60.4°
Best Local Similarity 63.2°
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 63.5
Best Local Similarity 60.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C,Accession: 150159
R;Cox, J.V.; Lazarides, E.
Mol. Cell. Biol. 8, 1327-1335, 1988
A,Title: Alternative primary structures in the transmembrane domain of the chicken eryth A;Reference number: 150159; MUID:88216609; PMID:2835670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 4-707, 'X', '709-902 <RES>
A; Cross references: GB:002756; NID:g192136; PIDN:AAA37278.1; PID:g553874
A; Cross references: GB:002756; NID:g192136; PIDN:AAA37278.1; PID:g553874
B; Demuth, D.R.; Showe, L.C.; Ballantine, M.; Palumbo, A.; Fraser, P.J.; Cioe, L.; Rovera
BRBO J. 5, 1206-1214, 1986
A; Title: Cloning and structural characterization of a human non-erythroid band 3-like pr
A; Reference number: A91039; MUID:86274622; PMID:3015590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Introns: 5/3; 46/1; 70/3; 131/1; 176/2; 217/3; 245/1; 305/3; 376/1; 447/1; 496/3; 561/
C;Superfamily: band 3 anion transport protein
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                          A; Molecule type: mRNA
A; Residues: 1-929 < KKOP>
A; Cross references: GB: XO2677; NID: 949897; PIDN: CAA26506.1; PID: 949898
A; Cross references: GB: XO2677; NID: 949897; PIDN: CAA26506.1; PID: 949898
A; Cross references: GB: XO2677; NID: 949897; PIDN: CAA26606.1; PID: 949898
A; Title: Structure of the murine anion exchange protein.
A; Reference number: A26086; MUD: 86034211; PMID: 3840489
A; Recession: A26086
A; Molecule Type: mRNA
A; Residues: 1-929 < KKO2
A; Residues: 1-929 < K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Ĝallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M19496; NID:g211211; PIDN:AAA48604.1; PID:g211212 C;Superfamily: band 3 anion transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 11-466,'S',468-929 <DEM>
A;Cross-references: GB:X03917; NID:953042; PIDN:CAA27555.1; PID:953043
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 929,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 92.7%; score 89; DB 2; Length 92;
Best Local Similarity 95.0%; Pred. No. 1.3e-05;
Matches 19; Conservative 0; Mismatches 1; Indels
                                 A; Reference number: A25314; MUID:85268011; PMID:2410791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 61; DB 2;
Pred. No. 0.25;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||::|| | |||||||:
|GKSAVPGERAHIVEVKEQRL 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GKASTPGAAAQIQEVKEORI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GKASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anion transporter - chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-844 <COX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
hes 12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SULT 4
```

οχ g A30816 band 3 anion transport protein (clone pBIIIC1) - chicken

g

<u>()</u>5

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

US-10-087-464-4 112 1 DRILLLFKPPKYHPDVPYVK 20 Title: Perfect score: edneuce:

BLOSUM62 Gapop 10.0 , Gapext 0.5 coring table:

283308 seqs, 96168682 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	3 anton	n (•	_	m	3 protein,	3-related	3-related		anion exchange pro	anion exchanger 3,	band 3-related pro	erythrocyte anion	probable sodium bi	hypothetical prote	sodium bicarbonate		ď	m	3 anion t			acid phosphatase (Na+ bicarbonate co	probable histone d	hypothetical prote	methylaspartate am	sporulation specif	sodium bicarbonate
D O	1		A25314			A25104		A31789					A33638												B75095			C96940	T13
ength DB	911 1						1234 2			1240 2			1227 2								336 1					335 1	~	5	
å Query Match Length	100.0	96.4	96.4	73.2	73.2	66.1	66.1	66.1	66.1	66,1	60.7	60.7	60.7	58.9		56.2		44.6		4	ω.	43.8	<u>_</u>			~	~		· ~
Score	112	108	108	82	82	7.4	7.4	74	74	74	89	89	989	99	99	63	62	20	50	50	4	49	49	49	4.8	4.8	4.8	4.8	48
Result No.	1	7	9	4		9	۰ ۲	- α	σ	10	11	12	13	14	15	16	17	60	19	20	21	22	23	24	25	26	27	200	53
																									,	y)	ı	4	

sodium bicarbonate sodium bicarbonate	conserved hypothet transglutaminase t	acid phosphatase (hypothetical prote	hypothetical prote	replicative DNA he	hypothetical prote	hypothetical prote	alpha 2,6-stalyltr	beta-galactoside a	beta-galactoside a	acid phosphatase (nodule-specific hy
T14110 T14031	F69019 B84146	T04599	T30143	E72237	G82329	T23748	AH1642	C42327	A28451	A41734	A59201	S11967
7 7	0 0	٦,	4 (7	7	~	7	~	~	7	7	٦	7
1035	234	466	137	306	468	1156	77	214	403	406	431	434
42.9	42.0	42.0	41.1	41.1	41.1	41.1	40.6	40.2	40.2	40.2	40.2	40.2
4 4 8	47	74	4 4	46	46	46	45.5	45	45	45	45	4.5
30 31	32	34.	3.5	37	38	36	40	41	42	4.3	44	45

ALIGNMENTS

•	RESULT 1
	band 3 anion transport protein, erythrocyte - human N,Alternate names: carrier family 4, anion exchanger, member 1; erythroid anion excha
	C; Species: Homo sapiens (man) C; Date: 03-Aug-1984 #sequence_revision 03-Oct-1995 #text_change 22-Jun-1999 C; Date: 03-Aug-1984 #sequence_revision 03-Oct-1995 #text_change 22-Jun-1999
	C; Accession: A36218; S03074; I39408; I39409; A92227; A20307; A32430; A30323; A20073; R; Lux, S.E.; John, K.M.; Kopito, R.R.; Lodish, H.F.
	Proc. Natl. Acad. Sci. U.S.A. 86, 9089-9093, 1989 A;Title: Cloning and characterization of band 3, the human erythrocyte anion-exchange
	A;Reference number: A36218; MUID:90083213; PMID:2594752 A:Accession: A36218
	A. Molecule type: mRNA
	A, Residues: 1-911 <lux></lux>
	A; Tanner, M.J.A.; Martin, P.G.; High, S.
_	Biochem. J. 256, 703-712, 1988 A:Title: The complete amino acid sequence of the human erythrocyte membrane anion-tr
	A; Reference number: S03074; MUID:89134172; PMID:3223947
	A; Accession: 8030/4 A.Molecule fune mRNA
	A, Residues: 1-55, 'E', 57-911 <tan></tan>
	A:Cross_references: EMBL.X1509; NID:928113; PIDN:CAA31128.1; PID:928/14
	A, Title: Localization of the gene for the erythroid anion exchange protein, band 3 (
	A,Reference number: 139408; MulD:88031311; PMID:34/0430 h.a.nossainn: 134408
	A: NOTECULE TYPE: DNA
	A; Residues: 37-56 <sho1></sho1>
	A/CIOSSITEMENTOSION (MINISTORIO) ALCONIO ALCON
	A; Molecule type: DNA
	A;Resdudes: 118-151
	R, Drickamer, L.K.
	J. Biol. Chem. 253, 7422-7484, 1948 a. mitter orientation of the band 3 polypeptide from human erythrocyte membranes. Ide
	A; Reference number: A92237; MUID: 79027186; PMID: 701248
	A.A.Ccession: A9.2.2.
	A; Residues: 1-3 <dri></dri>
	R.Mawby, W.J.; Findlay, J.B.C.
	Blockem. J. 203, 403-473, 1302 A;Title: Characterization and partial sequence of diriodosulphophenyl isothiocyanate
	A;Reference number: A26507; MUID:83074521; PMID:7150220 A:Acression: A26507
	A; Molecule type: protein
	R; Kaul, R.K.; Murthy, S.N.P.; Reddy, A.G.; Steck, T.L.; Kohler, H.
	J. Biol. Chem. 258, 7981-7990, 1983

A 60

```
A33810

band 3 anion transport protein - rat
C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 20-Aug-1999
C; Accession: A33810
C; Accession: A33810
J: Biol. Chem. 264, 8185-8192, 1989
A; Title: Primary structure of the rat kidney band 3 anion exchange protein deduced fine A; Reference number: A33810; MUID:89255254; PMID:2722777
C;Comment: Band 3 has at least two functional domains. Its integral domain mediates a ing sites for cytoskeletal proteins, glycolytic enzymes, and hemoglobin.
                                                                                                                                                                                                    A;Cross-references: GDB:119874; OMIM:109270
A;Map position: 17q21-17q22
C;Superfamily: band 3 anion transport protein
C;Superfamily: band amino end; glycoprotein; ion transport; phosphoprotein; transf F;1-403/Region: cytoskeletal protein binding
F;1-403/Region: anion antiporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 20-Aug-1999
C;Accession: A25314, A26086; I49524; B25104
R;Kopito, R.R.; Lodish, H.F.
Nature 316, 234-238, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB;U04793; NID:g203092; PIDN:AAA40800.1; PID:g203093 C;Superfamily: band 3 anion transport protein C;Keywords: alternative colling colling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Met) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     site: anion (Lys) #status experimenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <TM10>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <TM06>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <TM09>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <TM12>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 108; DB 2; Pred. No. 2.1e-08; 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 112; DB 1;
Pred. No. 5.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          predicted
predicted
predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           predicted
predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transmembrane #status
transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transmembrane #status
transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;861-881/Domain: transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acetylated amino end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DRILLERPPKYHPDVPYVK 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DRILLLFKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DRILLEKPPKYHPDVPYVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 20, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-848 <KUD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                590,851/Binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         642/Binding site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: A33810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;1/Modified site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;405-427/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    435-457/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       491-507/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-542/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;785-806/Domain:
F;839-859/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        459-479/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F; 568-588/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;604-624/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;659-680/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;701-721/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;723-743/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;764-780/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A25314
band 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
A; Molecule type: protein
A; Residues: 361-372:390-399; 604-613; 632-639; 647-656; 699-729; 731-743; 761-781; 818-826 «KAN
A; Experimental source: erythrocyte
A; Residues: 361-372:390-399; 604-613; 632-639; 647-656; 699-729; 731-743; 761-781; 818-826 «KAN
A; Experimental source: erythrocyte
A; Note: sequence extracted from NCBI backbone (NCBIP:113819, NCBIP:113821, NCBIP:113823,
A; Note: sequence extracted from NCBI backbone (NCBIP:113819, NCBIP:113821, NCBIP:113823,
A; Note: R; Kang, D.; Hamasaki, N.; Jennings, M.L.
A; Reference number: A49717; MUID:94124538; PMID:8294441
A; Reference number: A49717; MUID:94124538; PMID:8294441
A; Residues: 427-436; 479-519; 538-540; 559-566; 809-817; 825-841; 849-857 «OKU»
A; Note: Lys-539 and Lys-851 were shown to bind the same molecule of the anion transport
B; Hamasaki, N.; Okubo, K.; Kuma, H.; Kang, D.; Yae, Y.
J: Blochem: 122, 577-585, 1997
A; Title: Proteclytic cleavage sites of band 3 protein in alkali-treated membranes: Fidel
                                                                                       A. McCession: A92430
A. Molecule type: protein
A. M. J. 213. For Sep. 19. MUD: 83308584; PMID: 6615451
A. Reference number: A90323; MUD: 83308584; PMID: 6615451
A. Accession: A90323
A. Molecule type: protein
A. Residues: 559-630 CBRO>
A. Multiple: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Mesiduces: 1-55, Ev. 57-69 < YAN2>
A; Mesiduces: 1-55, Ev. 57-69
A; Mote: sequence extracted from NCBI backbone (NCBIP:49829)
A; Note: sequence of a common polymorphic form designated band 3 Memphis
B; Kang, D; Okubo, K.; Hamasaki, N.; Kuroda, N.; Shiraki, H.
A; Chem. 267, 19211-19217, 1992
A; Mote: A structural study of the membrane domain of band 3 by tryptic digestion. Configuracinc number: A44116; MUID:92406862; PMID:1527044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: A35835
A;Status: preliminary
A;Status: preliminary
A;Olecule type: protein
A;Residues: 361-364, 7X', 366-372;424-429, 7X', 431-434 <COB>
A;Note: Lys-430 is labeled by eosinyl-5-maleimide (EMA) in intact erythrocytes
A;Note: Lys-430 is labeled by eosinyl-5-maleimide (EMA) in intact erythrocytes
B;Vannoukanos, D.; Vassaur, C.; Driancourt, C.; Blouquit, Y.; Delaunay, J.; Wajcman, H.;
B;Dood 78, 1117-1120, 1991
A;Title: Human erythrocyte band 3 polymorphism (band 3 Memphis): characterization of the
A;Reference number: A44933; MUID:91329825; PMID:1678289
A;Accession: A44933
A;Accession: A44933
A;Accession: A44933
A;Residues: 1-55, E', 57-69 <XAN2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Primary structure of the cytoplasmic domain of human erythrocyte protein band 3 A;Reference number: S05523, MUD:90001294; PMID:2790053 A;Accession: S05523 MUD:90001294; PMID:2790053 A;Accession: S05523 MUD:90001294; PMID:2790053 A;Accession: S05523 MUD:90001294; PMID:2790053 A;Accession: S05523 MUD:90001294; PMID:2790053 A;Accession: A;Beth, A.H. Bibliochamistry 29, 8283 8290, 1990 A;Title: Identification of the eosinyl-5-maleimide reaction site on the human erythrocyt A;Reference number: A35835; MUD:91070049; PMID:1701324
     :Title: Amino acid sequence of the N(alpha)-terminal 201 residues of human erythrocyte Reference number: A92430; MUID:83238395; PMID:6345535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein date of the protein date of the protein states and shown to bind the affinity label pyridoxal phosphate, a substrate protein as both the diffinity label pyridoxal phosphate, a substrate promise of the protein substrate protein subplys. Acta 998, 43.49, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: PC4403
```

A; Title: Primary structure and transmembrane orientation of the murine anion exchang

ent: Band 3 is the major integral glycoprotein of the erythrocyte membrane. A dimd

61-911

~ c0

```
Dand 3-relateu protein - - and C. Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-U1-1990 #sequence_revision 20-Jul-1990 #text_change 20-Aug-1999
C;Date: 20-U1-1990 #sequence_revision 20-Jul-1990 #text_change 20-Aug-1999
C;Date: 20-U1-1990 #sequence_revision 20-Jul-1990 #text_change 20-Aug-1999
C;Accession: Ray911; A35770
A;Title: CDNA cloning and tissue distribution of mRNAs for two proteins that are rel
A;Recerence number: A34911; MUID: 90094439; PMID: 2294114
A;Accession: A34911
A;Status: preliminary
A;Accession: A34911
A;Status: preliminary
A;Accession: A34911
A;Residues: 1-1234 <kUD>
A;Residues: 1-1234 <kUD>
A;Residues: 1-1234 <kUD>
A;Coss-references: GB:J05166; NID: 9203090; PIDN: AA40799.1; PID: 9203091
A;Coss-references: GB:J05166; NID: 9203090; PIDN: AA40799.1; PID: 9203091
A;Title: Functional expression and subcellular localization of an anion exchanger C)
A;Reference number: A35770; MUID: 90319095; PMID: 2371270
                                                                                             C) Accession: A30816
R) Kim, H.R.C.; Yew, N.S.; Ansorge, W.; Voss, H.; Schwager, C.; Vennstroem, B.; Zenke, R) Kim, H.R.C.; Yew, 18. (416-4424, 1988
A) Title: Two different mRNAs are transcribed from a single genomic locus encoding the A; Reference number: A30816; MUD:89039870; PMID:318555
A) Accession: A30816
A; Molecule type: mRNA
A; Residues: 1-922 < MINA
A; Residues: 1-922 < 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: A25104
R;Demuth, D.R.; Showe, L.C.; Ballantine, M.; Palumbo, A.; Fraser, P.J.; Cioe, L.; Roy EMBO J. 5, 1205-1214, 1986
A;ritle: Cloning and structural characterization of a human non-erythroid band 3-likk A;Reference number: A91039; MUID:86274622; PMID:3015590
A;Accession: A25004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptua. A;Molecule type: mRNA A;Residues: 1-205,'A',207-924,'PG',927-1017,'IV',1020-1155,'ID',1158-1234 <LIN>C;Superfamily: band 3 anion transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            two proteins that are rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Residues: 1-205,'A',207-924,'PG',927-1017,'IV',1020-1155,'ID',1158-1234; Superfamily: band 3 anion transport protein
C.Species: Gallus gallus (chicken)
C;Date: 01-Dec-1989 #sequence_revision 30-Sep-1991 #text_change 16-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIDN:CAA27556.1; PID:g32121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 82; DB 2; Le. Pred. No. 0.00022; ); Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein, nonerythroid (MEB3) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 74; DB 2;
Pred. No. 0.0034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A) Residues: 1-865 < DENY
A) Residues: 1-865 < DENY
A) Cross-references: GB:X03918; NID:g32120; PID
C.Superfamily: band 3 anion transport protein
C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M23404
C;Superfamily: band 3 anion transport protein
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ERLHLLLMPPKHHPDVTYVK 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DRILLLFKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DRILLLLMPPKYHPKEPYV 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DRILLEKPPKYHPDVPYV 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.1%;
65.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 73.2%;
Best Local Similarity 78.9%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         band 3-related protein 2 - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 66.1
Best Local Similarity 65.0
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ρp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A tus; preliminary; translated from GB/EMBL/DDBJ
A tus; preliminary; translated from GB/EMBL/DDBJ
A) cuile type: DNA
A) didues: 4-707, 'X', 709-902 <RES>
A) cross-references: GB:J02756; NID:g192136; PIDN:AAA37278.1; PID:g553874
A) Cross-references: GB:J02756; NID:g192136; PIDN:AAA37278.1; PID:g553874
B) CB commuth, D.R.; Showe, L.C.; Ballantine, M.; Palumbo, A.; Fraser, P.J.; Cioe, L.; Rovers
EMBO J. 5, 1205-1214, 1986
A; Title: Cloning and structural characterization of a human non-erythroid band 3-like pr
A; Reference number: A91039; MUID:86274622; PMID:3015590
A; Rocession: B25104
A; Rosidues: 11-466, 'S', 468-929 <CDEM>
A; Rosidues: 11-466, 'S', 468-929 <CDEM>
A; Cross-references: GB:X03917; NID:g53042; PIDN:CAA27555.1; PID:g53043
C; Genetics: 5/3; 46/1; 70/3; 131/1; 176/2; 217/3; 245/1; 305/3; 376/1; 447/1; 496/3; 561/C; Superfamily: band 3 anion transport protein
C; Reywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.Cox. J.V.; Lazarides, E. Mol. Cell. Biol. 8, 1327-1335, 1988
Mol. Cell. Biol. 8, 1327-1335, 1988
A;Title: Alternative primary structures in the transmembrane domain of the chicken eryth A;Reference number: 150159; MUID:88216609; PMID:2835670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              apin transporter - chicken
cles: Gallus gallus (chicken)
cles: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Aug-1999
C;Accession: I50159
R;Cox, J.V.; Lazarider F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-844 <COX>A;Residues: 1-844 <COX>A;COXS-references: GB:M19496; NID:g211211; PIDN:AAA48604.1; PID:g211212 C;Superfamily: band 3 anion transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: A26086
A; Molecule type: mRNA
A; Residues: 1-929 < KRO2>
A; Residues: 1-929 < KRO2>
A; Cross-references: GB: M29379; NID:g191741; PIDN:AAA37187.1; PID:g191742
B; Kopito, R.R.; Andersson, M.; Lodish, H.F.
B; Biol. Chem. 262, 8032-8040; 1987
A; Title: Structure and organization of the murine band 3 gene.
A; Reference number: 149524; MUID:87250387; PMID:3036795
                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-929 < KODP>
A; Cross references: GB:X02677; NID:g49897; PIDN:CAA26506.1; PID:g49898
A; Cross references: GB:X02677; NID:g49897; PIDN:CAA26506.1; PID:g49898
B; Kopito, R.R.; Lodish, H.F.
J. Cell. Blochem. 29, 1-17, 1985
A; Title: Structure of the murine anion exchange protein.
A; Reference number: A26086; MUID:86034211; PMID:3840489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 108; DB 2; Length 92
Pred. No. 2.3e-08;
!: Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
    A; Reference number: A25314; WUID:85268011; PMID:2410791
A; Accession: A25314
```

1; Mismatches

96.4%; 95.0%;

Local Similarity 95.0 nes 19; Conservative

Best Loc Matches

d

A30816 band 3 anion transport protein (clone pBIIIC1) - chicken

Score 82; DB 2; Pred. No. 0.0002; 0; Mismatches 4

Query Match 73.2%; Best Local Similarity 78.9%; Matches 15; Conservative

A; Accession: I50159

S RESULT

1 DRILLLFKPPKYHPDVPYV 19

740

ò

Sequence 8, Appli Sequence 6266, Ap Sequence 6, Appli Sequence 3, Appli

Sequence 12 Sequence 12

Sequence

Appli

Sequence 7, A Sequence 1, A Sequence 9, A Sequence 12, Sequence 12, Sequence 12,

Sequence Sequence Sequence Sequence 6 Sequence 1, Appli Sequence 161, App

App1 i

Sequence

4, Appli 10360, A

Sequence 4,

Sequence Sequence

Sequence

Sequence

```
APPLICANT: Ob, Steven
APPLICANT: Ob, Steven
APPLICANT: Liu, David
APPLICANT: Goel, Vikas
APPLICANT: Li, Xuerons
APPLICANT: NUMBER: US/10/087,464
CURRENT APPLICATION NUMBER: US 06/272,930
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
2 US-10-017-161-2064

US-10-205-83-373

US-10-087-464-177

US-10-001-852-5

US-10-001-852-5

US-10-001-852-6

US-10-001-852-7

US-10-001-852-7

US-10-001-852-7

US-10-9-880-503-1

US-09-880-503-1

US-09-880-503-1

US-09-880-503-1

US-09-984-1186-12

US-10-237-667-12

US-10-237-666-12

US-10-237-661-12

US-10-237-661-12

US-10-237-661-12

US-10-237-661-12

US-10-237-661-12

US-10-237-661-12

US-10-237-661-12

US-10-237-661-12

US-10-237-661-12

US-10-237-681-12

US-10-237-681-12

US-10-237-681-12

US-10-31-81-11-14

US-09-880-503-6

US-09-880-503-6

US-09-880-503-6

US-09-880-503-6

US-09-880-503-6

US-10-311-82-161

US-10-313-656-4

US-10-133-656-4

US-10-133-656-4

US-10-133-656-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 104; DB 15;
Pred. No. 2.2e-09;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-108-605-355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
US-10-087 464-22
'S-quence 22, Application US/10087464
'Publication No. US20030059436Al
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/10087464
Publication No. US20030059436A1
GENERAL INFORMATION:
APPLICANT: Chishti, Ahar
APPLICANT: Oh, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 100.0%;
1 Similarity 100.0%;
20; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-087-464-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Appli
Sequence 22, Appl
Sequence 39328, A
Sequence 2, Appli
Sequence 6, Appli
Sequence 8, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 2, Appli
                                                                                                                                                                 (without alignments)
156.918 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2,
                                                                                                                                               September 3, 2003, 11:46:23; Search time 17.5 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / (gn2_6/ptodata/1/pubpaa/US07_PUBCOMB.ppp:*
/ (gn2_6/ptodata/1/pubpaa/US07_PUBCOMB.ppp:*
/ (gn2_6/ptodata/1/pubpaa/US06_NEW_PUB.ppp:*
/ (gn2_6/ptodata/1/pubpaa/US06_NEW_PUB.ppp:*
/ (gn2_6/ptodata/1/pubpaa/US07_NEW_PUB.ppp:*
/ (gn2_6/ptodata/1/pubpaa/US08_NEW_PUB.ppp:*
/ (gn2_6/ptodata/1/pubpaa/US08_NEW_PUB.ppp:*
/ (gn2_6/ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
/ (gn2_6/ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
/ (gn2_6/ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
/ (gn2_6/ptodata/1/pubpaa/US09_PUBCOMB.ppp:*
/ (gn2_6/ptodata/1/pubpaa/US09_NEW_PUB.ppp:*
/ (gn2_6/ptodata/1/pubpaa/US09_NEW_PUB.ppp:*
/ (gn2_6/ptodata/1/pubpaa/US09_NEW_PUB.ppp:*
/ (gn2_6/ptodata/1/pubpaa/US09_NEW_PUB.ppp:*
/ (gn2_6/ptodata/1/pubpaa/US09_NEW_PUB.ppp:*
/ (gn2_6/ptodata/1/pubpaa/US00_NEW_PUB.ppp:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
                          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-087-464-1
US-10-087-464-22
US-09-864-761-39328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-066-320-2

US-10-087-464-6

US-10-087-464-8

US-09-728-137-4

US-09-728-137-2

US-09-728-137-2

US-09-734-690-4
                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-920-804-2
US-09-920-804-4
US-09-734-674-2
US-10-274-990-2
                                                                                                                                                                                                                                                                                                                                                                   513375 seqs, 137303645 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                            US-10-087-464-1
104
1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115
115
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1032
1044
1085
1085
1088
1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1000.0
1000.0
1000.0
63.5
63.5
63.5
63.5
63.5
63.5
63.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                Perfect score:
                                                                                                                                                                                                                                                                                                             Scoring table:
```

Database :

Searched:

Sequence:

Run on:

ö

Gaps

.; 0

Result о В

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 911;
                                                                                                                                                                                                                                                                                                                       INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
INFORMATION: SWISSPROT HIT: P02730, EVALUE 3.00e-21
INFORMATION: EST_HUMAN HIT: BF526005.1, EVALUE 3.00e-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gomera, Andrew J.
APPLICANT: Singel, David J.
TITLE OF INVENTION: Method for Determining Physiological
FILE REFERENCE: 1818.1030-003
CURRENT PELLING NUMBER: US/10/066,320
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: PCT/US00/21101
PRIOR APPLICATION NUMBER: US60/146,680
PRIOR FILING DATE: 1999-08-02
NUMBER OF SED ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
       PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 39328
LENGTH: 86
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           core 104; DB 15;
red. No. 1.1e-07;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 104; DB 9;
Pred. No. 9.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 720 GMPWLSATTVRSVTHANALT 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/10066320
Publication No. US20030022267A1
GENERAL INFORMATION:
APPLICANT: Stamler, Jonathan S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S-10-087-464-6
Sequence 6, Application US/10087464
Publication No. US20030059436A1
GENERAL INFORMATION:
APPLICANT: Chishti, Athar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 GMPWLSATTVRSVTHANALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
illarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                         OTHER INFORMATION: BOTHER INFORMATION: EOTHER INFORMATION: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-864-761-39328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-066-320-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                 APPLICANT: Li, Xueros

TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
FILE REFERENCE: S1237/7019
CURRENT APPLICATION WUMBER: US/10/087,464
CURRENT APPLICATION WUMBER: US/02-03-01
PRIOR FILING DATE: 2002-03-02
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.0
SEQ ID NO 22
LENGTH: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica.X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           ; DB 15;
4.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DR FILING DATE: 2000-05-26

DR APPLICATION NUMBER: 05 09/632,366

DR APPLICATION NUMBER: 08 24263.6

DR FILING DATE: 2000-10-04

DR FILING DATE: 2000-10-04

DR FILING DATE: 2000-09-27

DR APPLICATION NUMBER: 05 00/236,359

DR APPLICATION NUMBER: 05 00/236,359

DR APPLICATION NUMBER: 05 00/236,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURKENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR PLICATION UNMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2001-01-30
PPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US01/00665 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US01/00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7-PRIOR APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 39328, Application US/09864761 Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 20; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-01-30
Chishti, Athar
                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapien
US-10-087-464-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dp
```

ij

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 66; DB 9; Length 1032;
Pred. No. 0.081;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.5%; Score 66; DB 9; Length 714; 57.9%; Pred. No. 0.056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
CURRENT FILING DATE: 200-12-01
PRIOR APPLICATION NUMBER: US/09/728,137
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: 09/115,954
PRIOR FILING DATE: 1998-07-15
PRIOR PLICATION NUMBER: EP 97401714.7
PRIOR PLICATION NUMBER: EP 97401713.9
PRIOR PLICATION NUMBER: EP 9840027.5
PRIOR FILING DATE: 1998-02-09
PRIOR PLICATION NUMBER: EP 98400454.9
PRIOR APPLICATION NUMBER: EP 98400454.9
PRIOR APPLICATION NUMBER: EP 98400454.9
PRIOR FILING DATE: 1998-02-06
PRIOR APPLICATION NUMBER: EP 98400454.9
PRIOR FILING DATE: 1998-02-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: GH-30409-D1
CURRENT APPLICATION NUMBER: US/09/728,137
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: 09/115,954
PRIOR FILING DATE: 1998-07-15
PRIOR FILING DATE: 1997-07-16
PRIOR FILING DATE: 1997-07-16
PRIOR APPLICATION NUMBER: EP 97401714.7
PRIOR FILING DATE: 1997-07-16
PRIOR APPLICATION NUMBER: EP 97401713.9
PRIOR FILING DATE: 1997-07-16
                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: EP 98400272.5 PRIOR FILING DATE: 1998-02-09 PRIOR PLICATION NUMBER: EP 98400454.9 PRIOR FILING DATE: 1998-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Antoine Michel Alain Bril
APPLICANT: Nassirah Khandoudi
APPLICANT: Xavier Martin
APPLICANT: Steven Charles Jupe
APPLICANT: Christopher John Rawlings
APPLICANT: Trudy Rachel Doe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:|| | || |:|| |:|
509 GLPWFVAATVLSITHVNSL 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/09728137
Patent No. US20010029031A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GMPWLSATTVRSVTHANAL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GMPWLSATTVRSVTHANAL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 63.5%;
Best Local Similarity 57.9%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Walter F. Boron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 57.9
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: HOMO SAPIENS
US-09-728-137-8
                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Fast
SEQ ID NO 8
LENGTH: 1032
                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 4
LENGTH: 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-728-137-8
                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-728-137-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             οy
                                                                    TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof FILE REFERENCE: $1237/7019
CURRENT APPLICATION NUMBER: US/10/087,464
CURRENT FILING DATE: 2002-03-01
PRIOR FILING APPLICATION NUMBER: US 06/272,930
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.0
LENGTH: 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Oh, Steven
APPLICANT: Liu, David
APPLICANT: Liu, David
APPLICANT: Goel, Vikas
APPLICANT: Li, Xuerong
TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
FILE REFERENCE: S1237/7019
CURRENT APPLICATION NUMBER: US/10/087,464
CURRENT FILING DATE: 2002-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                        Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 104; DB 15;
100.0%; Pred. No. 1.1e-07;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                        Score 104; DB 15;
Pred. No. 1.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 06/272,930 PRIOR FILING DATE: 2001-03-02 NUMBER OF SEQ ID NOS: 59 SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Xavier Martin
APPLICANT: Steven Charles Jupe
APPLICANT: Christopher John Rawlings
APPLICANT: Trudy Rachel Doe
TITLE OF INVENTION: NOVEL COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antoine Michel Alain Bril
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           720 GMPWLSATTVRSVTHANALT 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09728137
Patent No. US200100029031A1
GENERAL INFORMATION:
APPLICANT: Walter F. Boron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/10087464 Publication No. US20030059436A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; S. Best Local Similarity 100.0%; P. Matches 20; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nassirah Khandoudi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Chishti, Athar
       Liu, David
Goel, Vikas
Li, Xuerong
                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-464-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-087-464-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-087-464-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
US-09-728-137-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
LENGTH: 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-09-920-804-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: WEI, Ming-Hui et al
TITLE OF INVENTION: INCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THERROF
FILE REFERENCE: CLOO1018
CURRENT APPLICATION NUMBER: US/09/734,674
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 63.5%; Score 66; DB 9; Length 1044; Best Local Similarity 57.9%; Pred. No. 0.082; Matches 11; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 63.5%; Score 66; DB 9; Length 1085;
1 Similarity 57.9%; Pred. No. 0.085;
11; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                         APPLICANT AUCOINE MICHEL AGAIN BILL
APPLICANT Xavier Martin
APPLICANT Staven Charles Jupe
APPLICANT Christopher John Rawlings
APPLICANT Christopher John Rawlings
APPLICANT Trudy Rachel Doe
TITLE OF INVENTION NOVEL COMPOUNDS
FILE REFERENCE: GH-30409-D1
CURRENT APPLICATION NUMBER: 09/115,954
PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: EP 97401714.7
PRIOR APPLICATION NUMBER: EP 97401713.9
PRIOR APPLICATION NUMBER: EP 97401713.9
PRIOR FILING DATE: 1997-07-16
PRIOR FILING DATE: 1997-07-16
PRIOR FILING DATE: 1998-02-09
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 10
                                                   Sequence 2, Application US/09728137
Patent No. US20010029031A1
GENERAL INFORMATION:
APPLICANT: Walter F. Boron
APPLICANT: Antoine Michel Alain Bril
APPLICANT: Nassirah Khandoudi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             839 GLPWFVAATVLSITHVNSL 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09734674
Patent No. US20020081648A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:|| | || |:|| |:|
837 GLPWFVAATVLSITHVNSL 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GMPWLSATTVRSVTHANAL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GMPWLSATTVRSVTHANAL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-734-674-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: HOMO SAPIENS
US-09-728-137-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Fast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 4
LENGTH: 1085
RESULT 9
US-09-728-137-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-734-674-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   硆
```

RESULT 11

```
APPLICANT: WEI, MING-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: UNCLEEC ACID MOLECULES.ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001018 DIV
CURRENT APPLICATION NUMBER: US/210/274,990
CURRENT FILING DATE: 2002-10-22
PRIOR PAPLICATION NUMBER: 09/734,674
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Seino, Susumu; JCR Pharmaceuticals Co., Ltd.
TITLE OF INVENTION: Sodium Ion-Driven Chloride/Bi-Carbonate Exchanger FILE REFERENCE: GP44
CURRENT APPLICATION NUMBER: US/09/920,804
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09920804
Fatent No. US20020064846A1
Fatent No. US20020064846A1
GENERAL INFORMATION:
TITLE OF INVENTION: Sodium Ion-Driven Chloride/Bi-Carbonate Exchanger
FILE REPERENCE: GP4
CURRENT APPLICATION UNMBER: US/09/920,804
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 8
LENGTH: 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.5%; Score 66; DB 15; Length 1085; ilarity 57.9%; Pred. No. 0.085; Conservative 3; Mismatches 5; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.5%; Score 66; DB 9; 57.9%; Pred. No. 0.086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
Sequence 4, Application US/10274990 Publication No. US20030054491A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-920-804-2

Sequence 2, Application US/09920804

Patent No. US20020064846A1

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:|| | || |:|| |:|
840 GLPWFVAATVLSITHVNSL 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:|| | || |:|| |:|
837 GLPWFVAATVLSITHVNSL 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GMPWLSATTVRSVTHANAL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GMPWLSATTVRSVTHANAL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 63.5
Best Local Similarity 57.9
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapience US-09-920-804-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-920-804-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Mus musculus US-10-274-990-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 11; Conserv
```

```
US-09-734-674-2

US-09-734-674-2

Sequence 2, Application US/09734674

Sequence 2, Application US/09734674

Sequence 2, Application US/09734674

Sequence 2, Application US/09034674

Sequence 2, Application US/09046841

TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: AND USES THEREOF

TITLE OF INVENTION: NUMBER: US/09/734,674

CURRENT FILING DATE: 2000-12-13

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/10274990
Publication No. US20030054491A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
AND USES THEREOF
FILE REFERENCE: CL001018 DIV
CURRENT FILING DATE: 2002-10-22
PRIOR APPLICATION NUMBER: 09/734,674
PRIOR FILING DATE: 2002-110-22
RIOR APPLICATION NUMBER: 09/734,674
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 66; DB 15; Length 1129;
Pred. No. 0.089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 66; DB 9; Length 1129; Pred. No. 0.089;
Score 66; DB 9; Length 1088;
Pred. No. 0.086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                  |:||: | || |:|| |:|
840 GLPWFVAATVLSITHVNSL 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:|| | || |:|| |:|
881 GLPWFVAATVLSITHVNSL 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:|| | || |:|| 881 GLPWFVAATVLSITHVNSL 899
                                                                                         1 GMPWLSATTVRSVTHANAL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 63.5%; Soc
Best Local Similarity 57.9%; Pro
Matches 11; Conservative 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GMPWLSATTVRSVTHANAL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GMPWLSATTVRSVTHANAL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 63.5%;
Best Local Similarity 57.9%;
Matches 11; Conservative
  63.5%;
nilarity 57.9%;
Conservative
    Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Human
US-10-274-990-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Human
US-09-734-674-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 2
LENGTH: 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-274-990-2
                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                           δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
```

3, 2003, 11:53:43

Search completed: September Job time: 17.5 secs

```
GENERAL INFORMATION:
APPLICANT: BOTON, Walter F
APPLICANT: Bril, Antoine M
APPLICANT: Khandoudi, Nassirah
APPLICANT: Martin, Xavier
APPLICANT: Wavier
APPLICANT: Rawlings, Christopher J
APPLICANT: Doe, Trudy R
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30409
CURRENT APPLICATION NUMBER: US/09/115,954B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5, Appl
, Appli
8, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Appli
Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Appl
Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                   September 3, 2003, 11:42:58; Search time 15.75 Seconds (without alignments) 53.728 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 83, Sequence 84, Sequence 25, Sequence 25, Sequence 11, A Sequence 11, A Sequence 11, A Sequence 18, Sequence 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 62,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3,
Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1
Sequence 8
Sequence 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     328717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-115-954-8

US-09-734-674-4

US-09-734-674-4

US-09-734-674-2

US-09-101-272G-62

US-08-797-689-12

US-08-101-272G-80

US-09-101-272G-96

US-09-101-272G-96

US-09-101-272G-96

US-08-101-272G-96

US-08-101-272G-96

US-08-101-272G-98

US-08-101-272G-98

US-08-101-272G-98

US-08-101-272G-98

US-08-101-272G-98

US-08-101-272G-98

US-08-101-272G-98

US-08-101-272G-98

US-08-101-273G-98

US-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-07-942-157A-3
5219569-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-101-272G-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    328717 segs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                  1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                US-10-087-464-1
104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                                                                                                                                                                                                                                  seguence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                 Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No.
```

00000000000000000000000000000000000000	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	44466666666666666666666666666666666666	ww.44440wwww.	44431 4432 7719 7719 7719 7719 7727 7727 7888 8888 8888 888 888 884 884	らこよ よ 1 1 4 4 4 2 3 4 5 4 4 4 4 4	5188829-1 US-08-560 US-09-252 US-07-943 US-08-347 US-09-252 US-09-252 US-08-459 US-08-459 US-09-2052 US-09-2052 US-09-2052 US-09-2052 US-09-2052 US-09-2052 US-09-2052 US-09-2052 US-09-2052 US-09-2052 US-09-2052 US-09-2052 US-09-2052 US-09-2052 US-09-2052 US-09-2052	5188829-1 US-08-560-098A-47 US-09-552-991A-24157 US-07-243-843-4 US-08-347-003-4 US-08-347-003-4 US-09-252-991A-25255 US-09-252-991A-25255 US-09-252-991A-17821 US-08-459-346-12 US-09-252-991A-28044 US-09-252-991A-28044 US-09-252-991A-28044	453 1117 1100 15525 821 821	Sequence Seq	. 5188829 47, Appl 2417, A 2417, A 4, Appli 2525, A 17821, A 112, Appl 12, Appl 12, Appl 12, Appl 12, Appl 12, Appl 17,
RESULT 1 US-054-4 Sequence 4, Applica- Sequence 4, Applica- GENERAL INFORMATION APPLICANT: BOLON, 1 APPLICANT: BAIL, A APPLICANT: Khandou- APPLICANT: MAILON, APPLICANT: MAILON, APPLICANT: MAILON, APPLICANT: MAILON, APPLICANT: BALLING APPLICANT: BALLING DATA FILE REFERENCE: GH CURRENT FILING DATA FARLIER APPLICATION CURRENT FILING DATA EARLIER APPLICATION SOFTWARE: PALCATION SOFTWARE: PALCATION SEALIER APPLICATION LENGTH: APPLICATION SOFTWARE: PALCATION SEALIER APPLICATION TYPE: PRT	ALL 1911-954-4 199-115-954-4 199-115-954-4 199-115-954-4 199-115-954-4 199-115-954-4 199-115-954-1	4, Application US/0911595 5. 6200776 NIFORMATION: THE BOTON, Walter F THE BOTON, Walter F THE BATIL, Antoine M THE Khandoudi, Nassirah THE Khandoudi, Nassirah THE MARTIN, Xavier THE DOO, THOUGH COMPOUN THE DOO, THOUGH COMPOUN THO DOO, THOUGH COMPOUN THE DOO, THOUGH COMPOUN TH	cation 5 Nu: Walt Walt, 7, Walt 7, Xav 5, Erudy 005, C 005, C 1, C 1, C 1, C 1, C 1, C 1, C 1, C 1	un US/0911 ter F ine M Nassirah var C Christoph C, R MA9 UWBER: EP 1997-07-1 1997-07-1	1911 Coph COMP 17-1 1 EP 17-1	15, 714	MENTS 954B		•	
Query Best Match Y b b ESULT S-09-1 Seque	Match Local S les 11 1 509 2 2 2 2 15-954 - It No. 6 6 11 16 16 16 16 16 16 16 16 16 16 16	E 2::1 0.0	63.5%; Conservative IPWLSATTVRSVTHANA PWFVAATVLSITHVNS	63.5 57.9 tive SVTHA SITHV SITHV	5%; 9%; ANAL : /NSL	Score 6 Pred. N 3; Mism 19	re 66; DB 3; Mismatches Mismatches	Length 7 5; Indel	714; sls 0;	Gaps
; GENERA	C INFO	RMATIC	:NC							

```
Query Match
63.5%; Score 66; DB 4;
Best Local Similarity 57.9%; Pred. No. 0.052;
Matches 11; Conservative 3; Mismatches
                                                                                                                                                    |:|| | | | |:|| |:|
837 GLPWFVAATVLSITHVNSL 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:|| | || |:|| |:|
881 GLPWFVAATVLSITHVNSL 899
                                                                                                                           1 GMPWLSATTVRSVTHANAL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GMPWLSATTVRSVTHANAL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|| | || |: | ::|
838 LPWYVAATVISIAHIDSL 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 MPWLSATTVRSVTHANAL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 44.4%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 5/...
Best Local 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: HOMO SAPIENS
US-09-136-652-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1129
                                                                                                                                                                                                                              RESULT 5
US-09-734-674-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-734-674-2
        US-09-734-674-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
                                                                                                                                                                     qq
                                                                                                                               õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09734674

Patent No. 6498022

GENERAL INFORMATION:
APPLICANT: WEI, MING-Hui et al
    TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
    TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
    TITLE OF INVENTION: AND USES THEREOF
    PILE REFERENCE: CL001018
                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                            Length 1032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; DB 3; Length 1044; 0.05;
                                                                                                                                                                                                                                                                   5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Indels
                                                                                                                                                                                                                            Score 66; DB 3;
Pred. No. 0.049;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BOTOD, Walter F
APPLICANT: BAIL, Antoine M
APPLICANT: Bril, Antoine M
APPLICANT: Khandoudi, Nassirah
APPLICANT: Martin, Xavier
APPLICANT: Martin, Xavier
APPLICANT: Martin, Xavier
APPLICANT: Wawlings, Christopher J
APPLICANT: Boy, Trudy R
TILE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30409
CURRENT FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
BARLIER APPLICATION NUMBER: EP97401714.7
EARLIER FILING DATE: 1997-07-16
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTH: 1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 66; DB 3 Pred. No. 0.05; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/734,674
UNDRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASKED for Windows Version 4.0
CURRENT FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: EP97401714.7
EARLIER FILING DATE: 1997-07-16
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09115954B Patent No. 6200776 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                |:|| | || |:|| |:|
827 GLPWFVAATVLSITHVNSL 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:|| | || |:|| |:|
839 GLPWFVAATVLSITHVNSL 857
                                                                                                                                                                                                                                                                                                           1 GMPWLSATTVRSVTHANAL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GMPWLSATTVRSVTHANAL 19
                                                                                                                                                                                                                            Query Match 63.5%;
Best Local Similarity 57.9%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 63.5%;
Best Local Similarity 57.9%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
US-09-115-954-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 4
LENGTH: 1085
                                                                                                                           LENGTH: 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-115-954-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-115-954-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-734-674-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
Sequence 2, Application US/09734674

Patent No. 649802

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: INCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/734,674
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2.0
                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1079;
Length 1085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.5%; Score 66; DB 4; 57.9%; Pred. No. 0.054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 47; DB 3;
Pred. No. 45;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09136652A

Patent No. 6096517

GENERAL INFORMATION:
APPLICANT: BRILL, ANTOINE
APPLICANT: HARDTIN, NASSIRAH
APPLICANT: MARTIN, XAVIER
TITLE OF INVENTION: WALTER
TITLE OF INVENTION: WOVEL COMPOUNDS
FILE REFERENCE: GP-30010
CURRENT APPLICATION NUMBER: US/09/136,652A
CURRENT APPLICATION NUMBER: US/09/136,652A
CURRENT FILING DATE: 1998-08-19
EARLIER PAPLICATION NUMBER: EP 974019473.3
SOFTWARE PAPLICATION NUMBER: EP 974019473.3
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
```

```
Gaps
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                  Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.3%; Score 43; DB 4; Length 194; 43.8%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INCORDATION:
GENERAL INCORDATION:
APPLICANT: Nissin Food Products Co., Ltd.
TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
FILE REPERENCE: 050979
CURRENT APPLICATION NUMBER: US/09/101,272G
PRIOR APPLICATION NUMBER: UP 1059/1996
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 107
SOCTWARE: Patentin version 3.1
SEQ ID NO 80
LENGTH: 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Nissin Food Products Co., Ltd.
TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
FILE REFERENCE: 050979
                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                               41.3%; Score 43; DB 43.8%; Pred. No. 18; tive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/101,272G
CURRENT FILING DATE: 1998-07-08
PRIOR APPLICATION NUMBER: JP 1059/1996
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin version 3.1
SEO ID NO 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: ATFHI chimeric protein US-09-101-272G-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature; OTHER INFORMATION: ATF domain of uPA US-09-101-2726-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 80, Application US/09101272G Patent No. 6509445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 73, Application US/09101272G
Patent No. 6509445
  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               :|| ||| :: ||:
75 LPWNSATVLQQTYHAH 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|| ||| :: ||:
73 LPWNSATVLQQTYHAH 88
                                                                                                                                                                                                                                                                                                                                      2 MPWLSATTVRSVTHAN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 MPWLSATTVRSVTHAN 17
                                       TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 43.8 Matches 7; Conservative
                                                                                                                                                                                                                                             Query Match 41.3
Best Local Similarity 43.8
Matches 7; Conservative
                                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-797-689-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
US-09-101-272G-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-101-272G-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 200
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Fleer, Reinhard
APPLICANT: Fournier, Alain
APPLICANT: Guitton, Jean-Dominique
APPLICANT: Guitton, Jean-Dominique
APPLICANT: Jung, Gerard
APPLICANT: Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                  ) NAME/KEY: misc_feature
; OTHER INFORMATION: residues 43-131 of the ATF domain of uPA
US-09-101-272G-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                               APPLICANT: NISSIN FOOD Products Co., Ltd.
TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
FILE REFERENCE: 050979
CURRENT APPLICATION NUMBER: US/09/101,272G
CURRENT FILING DATE: 1998-07-08
PRIOR PLICATION NUMBER: JP 1059/1996
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 41.3%; Score 43;
Best Local Similarity 43.8%; Pred. No.
Matches 7; Conservative 4; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY ASSETT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhone-Poulenc Rorer Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT/FR93/00085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/256,927 FILING DATE: 28-JUL-1994 APPLICATION NUMBER: FR 92/01064 FILING DATE: 31-JM-1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/FR93/0008
                  Sequence 62, Application US/09101272G Patent No. 6509445 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/08797689 Patent No. 5876969 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            500 Arcola Road, 3C43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|| ||| :: ||:
30 LPWNSATVLQQTYHAH 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 MPWLSATTVRSVTHAN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 28-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 3. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Collegeville
                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
US-09-101-272G-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-797-689-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                       SEQ ID NO 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
```

g δ

```
MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-746-682A-11
US-08-597-236-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
               Score 43; DB 4; Length 200; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.3%; Score 43; DB 4; Length 201; 43.8%; Pred. No. 27; tive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.3%; Score 43; DB 4; Length 208;
43.8%; Pred. No. 29;
tive 4; Mismatches 5; Indels
                                                       5; Indels
                                                                                                                                                                                                                                                                             APPLICATE: MISSIN FOOD PRODUCTS CO., Ltd.
TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
FILE REFERENCE: 620979
CURRENT APPLICATION NUMBER: US/09/101,272G
CURRENT FILING DATE: 1998-07-08
PRIOR APPLICATION NUMBER: JP 1059/1996
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Nissin Food Products Co., Ltd.
TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
FILE REPRENCE: Q50979
CURRENT APPLICATION NUMBER: US/09/101,272G
CURRENT FILING DATE: 1998-07-08
PRIOR APPLICATION NUMBER: JP 1059/1996
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEO ID NOS: 107
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: ATFHI-CL chimeric protein US-09-101-272G-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: ATFHI-ML chimeric protein US-09-101-2726-98
                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 98, Application US/09101272G; Patent No. 6509445; GENERAL INFORMATION:
                                                                                                                                                                                                          US-09-101-272G-96; Sequence 96, Application US/09101272G; Patent No. 6509445; GENERAL INFORMATION:
                                                                                                               :|| ||| : ||:
92 LPWNSATVLQQTYHAH 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :|| ||| : ||:
73 LPWNSATVLQQTYHAH 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 98
LENGTH: 208
TYPE: PT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :|| ||| : ||:
73 LPWNSATVLQQTYHAH 88
                                                                                           2 MPWLSATTVRSVTHAN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 96
LENCHH: 201
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 MPWLSATTVRSVTHAN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 MPWLSATTVRSVTHAN 17
               Query Match 41.3%;
Best Local Similarity 43.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O'ery Match
Best Local Similarity 43.8'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 41.3
Best Local Similarity 43.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
US-09-101-272G-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

RESULT 13

```
.;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Indels
Sequence 11, Application US/08597236
Fatent No. 5733765
GENERAL INFORMATION:
APPLICANT: STINGELE, Franscesca
APPLICANT: MOLLET, Beat
TITLE OF INVENTION: LACTIC BACTERIA PRODUCING
TITLE OF INVENTION: EXOPOLYSACCHARIDES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americans
                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/597,236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LACTIC BACTERIA PRODUCING
EXOPOLYSACCHARIDES
19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 54;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 1155 Avenue of the Americans
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/746,682A FILING DATE: 14-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/08746682A
Patent No. 5766184
GENERAL INFORMATION:
APPLICANT: STINGELE, Franscesca
APPLICANT: MOLLET, Beat
TITLE OF INVENTION: LACTIC BACTERIA
TITLE OF INVENTION: EXOPOLYSACCHARID
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: EP 95201669.9 FILING DATE: 20-JUN-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 MPWFILTVLATLFHATAI 177
                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 MPWLSATTVRSVTHANAL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 38.9%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Fanucci A., Allan
REGISTRATION NUMBER: 303
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                          CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 426
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New York : U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
```

ó

```
οy
                                                                                                                                                                                                                                        염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: WNENDT, STEPHAN

PPPLICANT: SCHNEIDER, JOHANNES

APPLICANT: HEINZEL-WIELAND, REGINA

APPLICANT: SAUNDERS, DEREK J.

TITLE OF INVENTION: BIFUNCTIONAL UROKINASE VARIANTS WITH

TITLE OF INVENTION: INPROVED FIBRINOLYTIC CHARACTERISTICS AND THROMBIN

TITLE OF INVENTION: INHIBITING EFFECT

NUMBER OF SEQUENCES: 83

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB 1; Length 360;
Pred. No. 54;
4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESEE: Evenson, McReown, Edwards & Lenahan STREET: 1200 G Street, N. W. Suite 700 CITY: Washington, D.C. COUNTRY: U.S. ZIP: 20005

COWITRY: U.S. ZIP: Toppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPOTER: IBM PC COMPATIBLE COMPATIBLE STREET: BOOF COMPATIBLE STREET: 20-JUL-1993

CLASSIFICATION NUMBER: US/08/093,741
FILING DATE: 12-JUL-1993

ATTORNEY AGENT INFORMATION: PILING DATE: 15-JUL-1993

ATTORNEY AGENT INFORMATION: NUMBER: DE P43 23 754.1
FILING DATE: 15-JUL-1993

ATTORNEY AGENT INFORMATION: NUMBER: DE P43 23 754.1
CLASSIFICATION: 435
PRIOR APPLICATION DATA
PRIOR APPLICATION NUMBER: 08/597,236
FILING DATE: 20-UN-1995
FILING DATE: 20-UN-1995
FILING DATE: 20-UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fannori A., Allan
REGISTRATION NUMBER: 30256
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: AMINORALING 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 83, Application US/08093741 Patent No. 5681721 GENERALINFORMATION: GENERALISANT: STEFFENS, GERD J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (202)628-8044
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 MPWFILTVLATLFHATAI 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 MPWLSATTVRSVTHANAL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (202)628-8800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 38.9%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
US-08-093-741-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-746-682A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-093-741-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ωp
```

41.3%; Score 43; DB 1; Length 365;

Query Match

```
Best Local Similarity 43.8%; Pred. No. 54;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps Qy 2 MPWLSATTVRSVTHAN 17

Db 26 LPWNSATULQTYHAH 41

Search completed: September 3, 2003, 11:52:26

Job time : 16.75 secs
```

Scoring table:

Searched:

Database :

Perfect score:

Sequence:

OM protein

Run on:

```
Human erythrocyte
A. tigrinum ABI pr
Human erythrocyte
Human Band 3 prote
Human Band 3 prote
Rovel human secret
Novel human secret
A. tigrinum AB2 pr
A. tigrinum AB2 pr
A. tigrinum AB2 pr
Drosophila melanog
                                                                                                                                                                                                                                Human secreted pro
Human secreted pro
Human secreted pro
Human heart muscle
                                                                                                                                                                                                                                                                               Human NT2-2A prote
Drosophila Na+ dri
Drosophila Na+ dri
Drosophila Na+ dri
Drosophila Na+ dri
                                                                                                                                                                                                                                                                                                                                                                                           Larval viability a
Human protein sequ
Human polypeptide
Human transporter
                                                                                                                                             hNBC3 protein sequ
Human brain-derive
Murine Na+-driven
                                                                                                                                                                                   Human Na+-driven C
                                                                                                                      hNBC3 protein sequ
                                                                                                                                     hNBC3a protein seq
                                                                                                                                                                                              Human transporter
Human transporter
                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine; protozoacide; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated Band 3 polypeptide which selectively binds to merozite surface protein-1, useful for the prevention and treatment of malarial infection
                                                                                                                                                                                                                                                                                                                                                         Drosophila
Drosophila
                                                                                                                                                                                                                                                                                                                                            Drosophila
                                                                                                                                                                                                                        Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SELI-) ST ELIZABETH'S MEDICAL CENT INC.
               AAW90263
AAB46914
AAE29343
                                                 AAE29344
AAU30825
AAP60645
AAW90262
AAW90261
ABB63733
                                                                                                                     AAW74410
AAW74409
AAW74408
AAB20659
                                                                                                                                                                     AAB47931
AAB47932
ABG32015
ABG32014
ABG303611
                                                                                                                                                                                                                                                        AAB28342
AAB11833
                                                                                                                                                                                                                                                                                 AAW90274
AAB23336
AAB23340
                                                                                                                                                                                                                                                                                                                   AAB23341
AAB23342
ABB60785
AAB23337
AAB23339
                                                                                                                                                                                                                                AAB28321
AAB28341
                                                                                                                                                                                                                                                                                                                                                                                            ABG70008
                                                                                                                                                                                                                                                                                                                                                                                                                    ABP69139
                                                                                                                                                                                                                                                                                                                                                                                                                               AAE22918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE29339 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002; 2002WO-US06415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-MAR-2001; 2001US-272930P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Band 3 peptide, B35A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                 779
779
1017
                                                                         292
11240
11239
11239
11039
11088
111088
11120
11120
1130
931
931
744
774
                                                                                                                                                                                                                                                                                                                                                      1030
1030
1086
1086
121
121
1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-759814/82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oh ss,
  WO200270542-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chisht AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-SEP-2002.
                                                                        104
104
104
104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE29339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE29339
   Human Band 3 pepti
Human Band 3 prote
Human liver peptid
Peptide #6645 enco
Protein #6029 enco
Human brain expres
Human bone marrow
Peptide #6670 enco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human peptide enco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                               September 3, 2003, 11:24:37 ; Search time 48.5 Seconds
(without alignments)
65.454 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                              ASIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
SIDISI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
SIDISI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
SIDISI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
SIDISI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
SIDISI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
SIDISI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
SIDISI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
SIDISI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
SIDISI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
SIDISI/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
SIDISI/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
SIDISI/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
SIDISI/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
SIDISI/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
SIDISI/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
SIDISI/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
SIDISI/gcgdata/geneseqp-embl/AA1991.DAT:*
SIDISI/gcgdata/geneseqg-embl/AA1991.DAT:*
SIDISI/gcgdata/geneseqg-embl/AA2001.DAT:*
SIDISI/gcgdata/geneseqg-embl/AA2001.DAT:*
SIDISI/gcgdata/geneseqg-embl/AA2001.DAT:*
SIDISI/gcgdata/geneseqg-embl/AA2001.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*
                                                                                                                                                                                                                                             1107863
             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                     1107863 segs, 158726573 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE29339
AAE29349
ABG54066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM72377
AAM32633
ABG42195
                                                            - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB24030
AAM59792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB39139
                                                                                                                                             104
1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                      A_Geneseq_19Jun03:*
                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3555555533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                   US-10-087-464-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0
100.0
100.0
100.0
100.0
100.0
```

Score

Š

1004 1004 1004 1004 1004

melanog Na+ dri Na+ dri

human diagno

~

ö

Gaps

;

42;

Length Indels

Score 104; DB 23; Pred. No. 5.1e-10; Mismatches

100.0%; 100.0%;

20

; 0

¥.

```
Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
sequence is human Band 3 protein ectoplasmic domain 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human liver peptide, SEQ ID No 32714.
                                                                                                                                                                                         1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                               ABG54066 standard; Peptide; 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                     1 GMPWLSATTVRSVTHANALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JUN-2000; 2000US-0608408.
31-SEP-2000; 2000US-0632566.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236559.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2001; 2001WO-US00664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0207456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                               25-FEB-2003 (first entry)
                                                                                                                          20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-488898/53.
                                                                                    Query Match
Best Local Similarity
                                           42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200157273-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                        ABG54066;
                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Penn SG,
                                                                                                                          Matches
                                                                                                                                                                                                                                                                        RESULT 3
                                                                                                                                                                                                                                                                                          ABG54066
                                                                                                                                                                     δλ
                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                     ö
                                                   The invention relates to an isolated Band 3 polypeptide that comprises any of 4 20 residue amino acid sequences, or their fragments that bind to an MSPP-1 polypeptide or a polypeptide with any of 8 291-131 base pair sequences. The methods and compositions of the present invention are useful for the prevention and treatment of malarial infection. The present invention, develops new and more improved methods based upon inhibiting the particular interactions between the malarial parasite and a cognate molecule present in the host and subsequently minimising harmful side effects and drug resistance that may be due to non specific therapeutic approaches. The invention is useful in gene therapy. The present invention also provides a vaccine for malaria. The present sequence is human Band 3 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated Band 3 polypeptide that comprises any of 4 20 residue amino acid sequences, or their fragments that bind to an MSP-1 polypeptide or a polypeptide with any of 8 291-131 base pair sequences. The methods and compositions of the present invention are useful for the prevention and treatment of malarial infection. The present invention, develops new and more improved methods based upon inhibiting the particular interactions between the malarial parasite and a cognate molecule present in the host and subsequently minimising them fills and drug resistance that may be due to non-specific therapeutic approaches. The invention is useful in gene therapy. The present invention also provides a vaccine for malaria. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated Band 3 polypeptide which selectively binds to merozite surface protein-1, useful for the prevention and treatment of malarial
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                            Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 104; DB 23;
100.0%; Pred. No. 2.1e-10;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Band 3 protein ectoplasmic domain 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SELI-) ST ELIZABETH'S MEDICAL CENT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goel V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE29349 standard; peptide; 42 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example; Page 58; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GMPWLSATTVRSVTHANALT 20
                   Claim 1; Page 84; 163pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-MAR-2001; 2001US-272930P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002; 2002WO-US06415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protozoacide; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 20, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oh ss,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-759814/82.
                                                                                                                                                                                                                                                                                                                                20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200270542-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chishti AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-SEP-2002.
                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE29349;
```

RESULT 2 AAE29349

ò

```
ö
                                                                                                                                                                                         The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the
                                                                                                                                                                                                                                                                                                              specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (1) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG59930 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human liver single exon encoded peptides of the invention.
Note: The sequence information for this patent does not appear in the
printed specification but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Human genome-derived single exon nucleic acid probes useful for analysing gene expression in human adult liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 104; DB 22; ilarity 100.0%; Pred. No. 1.2e-09; Conservative 0; Mismatches 0;
                                                                                                                 Claim 27; SEQ ID No 32714; 658pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity es 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
```

Rank DR;

Chen W,

 \sim

```
The present invention relates to single exon nucleic acid probes for measuring human peace expression in a sample derived from human heart (see ABA21535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, human section, cardiac arriththmiss and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human brain expressed single exon probe encoded protein SEQ ID NO: 31897.
            Protein #6029 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 86;
                                        Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 104; DB 22;
100.0%; Pred. No. 1.2e-09;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID No 25800; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                           Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM59792 standard; Protein; 86 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GMPWLSATTVRSVTHANALT
                                                                                                                                                                                                                                    2000US-0207456.
2000US-0608408.
2000US-0632366.
                                                                                                                                                                                                                                                                               2000US-0234687.
2000US-0236359.
2000GB-0024263.
                                                                                                                                                                                            2001WO-US00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 20; Conservative
                                                                      congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                           Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86 AA;
                                                                                                                                WO200157274-A2.
                                                                                                                                                                                                                                                                03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                     Homo sapiens.
                                                                                                                                                                                          30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                              04-OCT-2000;
                                                                                                                                                                                                                                    26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                        04-FEB-2000;
                                                                                                                                                              09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM59792;
                                                                                                                                                                                                                                                                                                                                                                           Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                     hearts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM59792
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                      Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                        Peptide #6645 encoded by human foetal liver single exon probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 27; SEQ ID NO 31774; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 104; DB 22;
100.0%; Pred. No. 1.2e-09;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB24030 standard; Protein; 86.AA.
                                                                                                                  ABB39139 standard; Peptide; 86 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 GMPWLSATTVRSVTHANALT: 53
              GMPWLSATTVRSVTHANALT 20
                             04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234587.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen W,
                                                                                                                                                                                                                                                                                                                                                           30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-JAN-2002 (first entry)
                                                                                                                                                                            04-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 AA;
                                                                                                                                                                                                                                                                                                WO200157277-A2
                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-OCT-2000;
                                                                                                                                                                                                                                                                                                                              09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB24030;
                                       34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
ABB24030
                                                                                                 ABB39139
                                                                                                                                  g
                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  XXXX
              ò
```

ö

Gaps

```
Hanzel DK,
                          Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-488897/53.
                                                                                                                                                                                                 Local Similarity
nes 20; Conserv
                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                         genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                           WO200157272-A2.
                                                                                                                                                                       98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-OCT-2000;
                                                                                                                                                                                                                                                                                                                             17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2001
                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                           AAM32633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SG,
                                                                                                                                                                                         Query Match
                          Penn SG,
                                                                                                                                                                                                                                                                                                                                                                Probe;
                                                                                                                                                                                                   Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Penn
                                                                                                                                                                                                                                                                        RESULT 8
                                                                                                                                                                                                                                                                                  AAM32633
염
                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                   The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                         Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; bone marrow expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human bone marrow expressed probe encoded protein SEQ ID NO: 32683
                                                                                                                                                                                                                   Example 4; SEQ ID NO: 31897; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                            Length 86;
                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                            100.0%; Score 104; DB 22; 100.0%; Pred. No. 1.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              microarray; cancer; leukaemia; lymphoma; myeloma
                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                       Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                            AAM72377 standard; Protein; 86 AA
                                                                                                                                                                                                                                                                                                                                                                         GMPWLSATTVRSVTHANALT 53
                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                               1 GMPWLSATTVRSVTHANALT
                                                                    26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632566.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-023559.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                      Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0180312.
2000US-0207456.
2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0632366.
2000US-0234687.
2000US-0236359.
2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001WO-US00668
                                            2001WO-US00667
                                                             2000US-0180312
                                                                                                                                                                                                                                                                                          the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 20, Conservative
                                                                                                                                                      Penn SG, Hanzel DK,
                                                                                                                                                                      WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                           86 AA;
        WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200157276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-2001;
                                           30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-2001
                          09-AUG-2001
                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                34
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM72377;
                                                                                                                                                                                                 brains
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                    AAM7237
ò
                                                                                                                                                                                                                                                                                                                                                                            Dp
```

```
The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide #6670 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                 Example 4; SEQ ID NO: 32683; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 104; DB 22;
100.0%; Pred. No. 1.2e-09;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                     analyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       analyzing gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 27; SEQ ID No 32902; 654pp; English.
                                                               Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen W, Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM32633 standard; Protein; 86 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MOLE-) MOLECULAR DYNAMICS INC
(MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GMPWLSATTVRSVTHANALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0207456.
2000US-0608408.
2000US-0632366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0234687.
2000US-0236359.
2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2001; 2001WO-US00663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
```

us-10-087-464-1.rag

```
Sequence
                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
  δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with mRNA, and (b) measuring the label detectably bound to each probe of
predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                             Human peptide encoded by genome-derived single exon probe SEQ ID 31860.
                                                                                                                                                                                                                                                                                                                                 Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histlocytosis; lymphagioleleomyomicosis; Karagener syndrome; pulmonary alveolar proteinnosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spatially-addressable set of single exon nucleic acid probes, used to
                                                                                          Gaps
                                                                                                                                                                                                                                                                                  Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                         ö
                                                                   Length 86;
                                                                                         Indels
                                                                  100.0%; Score 104; DB 22; 100.0%; Pred. No. 1.2e-09;
                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      measure gene expression in human lung samples
                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 27; SEQ ID No 31860; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rank DR;
                                                                                                                                                                                            ABG42195 standard; Peptide; 86 AA
                                                                                                              1 GMPWLSATTVRSVTHANALT 20
                                                                                                                             34 GMPWLSATTVRSVTHANALT 53
                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0632366.
2000US-234687P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-207456P.
2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US00665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-180312P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-236359P
                                                                                                                                                                                                                                         (first entry)
                                                                            Local Similarity 100.
Les 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                              hyaline membrane disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-114183/15.
                                             86 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            WO200186003-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAY-2000;
                                                                                                                                                                                                                                        19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-NOV-2001
                                              Sequence
                                                                                                                                                                                                                  ABG42195;
                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Penn SG,
                                                                                         Matches
                                                                                                                                                                     ABG42195
8
                                                                                                                                                                                                                    á
                                                                                                                                     셤
```

```
the array; identifying exons in a eukaryotic genome, comprising

(a) algorithmically predicting at least one exon from genomic sequences
of the eukaryote; and (b) detecting specific hybridisation of detectably
labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
having a fragment identical to the predicted exon, the probe is included
on the above mentioned microarray; assigning exons to a single gene,
comprising (a) identifying exons from genomic sequence by the method
above and (b) measuring the expression of each of the exons in several
tissues and/or cell types using hybridisation to a single exon
microarrays having a probe with the exon, where a common pattern of
expression of the exons in the tissues and/or cell types indicates that
the exons should be assigned to a single gene; a peptide comprising one
of 12011 sequences, mentioned in the specification, or encoded by the
probes/open reading frames (ORF). The probes are used for gene
expression analysis, and for identifying exons in a gene, particularly
using human lung derived mRNA and for the study of lung disease
(COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
tibromary alvoslar proteinosis, Karagener syndrome, sarcoidosis, pulmonary
hemann-Pick disease, Hermansky-budlak syndrome, sarcoidosis, pulmonary
hemann-Pick disease, Intervosis, Raragener syndrome, fibrocystic
pulmonary alvoslar proteinosis, Karagener syndrome, sarcoidosis, pulmonary
alvoslar proteinosis, Karagener syndrome, sarcoidosis,
and hyaline membrane disease. The present sequence is a peptide/protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic senescent cell antigen and peptide(s) - used to detect antibodies to SCA, study cellular ageing and auto-immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human erythrocyte membrane anion-transport protein (band 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Senescent cell peptide; ANION 1; COOH; auto immune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 104; DB 23; 100.0%; Pred. No. 1.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (RESE ) RESEARCH CORP TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR15355 standard; Protein; 911 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 GMPWLSATTVRSVTHANALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91WO-US03557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90US-0528210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kay MBM, Marchalonis JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1991-369184/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAQ15172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
08-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-NOV-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9118013-A.
```

ó

```
disorders mediated by NBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB46914;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB46914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ٠<u>;</u>
                                                                                     The amino acid sequence is that of the human erythrocyte anion-transport protein (band 3). Amino acids 538-554 (ANION 1) or 812-827 (COOH) code for a peptide which is immuno-reactive with antibodies to senescent cell antigen (SCA). The antigen and peptides can be used in any method or technique involving or requiring the inhibition of the binding of senescent cell ig to senescent cells in vitro or in vivo. The prods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NBC; sodium blearbonate transporter family; pH regulation; immunoassay; treatment; water retention; blood pressure; acidosis; inflammation; cell proliferation; cancer; sperm activation; inactivation; epilepsy; hydroencephaly; glaucoma; colitis; salamander; ABI; anion exchange.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                          Immunological mechanisms in humans and other animals, such as those relating to cellular ageing, degeneration, and life span; removal of senescent cells; anion transport across cellular membranes; disease mechanisms where increased senescent cell ig6 may play a role, such as haemolytic anaemia, sickle cell anaemia and idlopathic thrombotycopenia purpura; other autoinmune disease mechanisms, such as rheumatoid arthritis and systemic lupus erythematosus; and other specifically, the prods are useful in cosmetic and pharmaceutical compens. Adaptostic kits, and methods for detecting or measuring abs to SCA, studying cellular ageing and autoimmune mechanisms,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       separating anions from a gas or liquid, or diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid molecules encoding proteins of the Sodium Bicarbonate Cotransporter (NBC) family - useful for identifying agents that agonise or antagonise NBC activity and treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bevensee MO, Biemesderfer D, Boron WF;
is BA, Grichtchenko II, Romero MF, Schmitt BM;
  mechanisms, separate anions and treat auto-immune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 104; DB 12;
100.0%; Pred. No. 2.1e-08;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW90263 standard; peptide; 911 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        720 GMPWLSATTVRSVTHANALT 739
                                            Disclosure; Fig 1; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-US10297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0047131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
nes 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A. tigrinum AE1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aalkjaer C, Bevense
Choi I, Davis BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-059743/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ambystoma tigrinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9853067-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Choi I, Da
Sussman CR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               certain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW90263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW90263

LD AAW9

XX XX XX

DT 27-P

XX XX XX

DD A. t

XX XX

XX X

DD A. t

XX X

DD A. t

XX X

DD A. t

DD A. t

DD A. t

Color

DD Color

DD Color

Color

Color

Color

DD C
g
```

```
This sequence represents the anion exchange protein AEI which is used in a method resulting in the isolation of a novel salamander sodium bicarbonate transporter (NBC) NBC proteins and nucleic acid sequences may be used to treat pathological processes including water retention, increased blood pressure, chronic respiratory and metabolic acidosis, inflammation, cell proliferation, cancer, sperm activation/inactivation, hydroencephaly, epilepsy, glaucoma and colitis. Members of the NBC family of proteins can be used (i) as a target to identify agents that block or stimulate new mediated binding partners that bind NBC, (iii) in methods to identify and isolate binding partners that bind NBC, (iii) in methods to identify agents that block or stimulate activity of an NBC protein, and (iv) as a target to assay for NBC-mediated activity. Anti-NBC antibodies are also useful as modulators of NBC activity, useful in the immunoassays for detecting NBC expression/activity and for purifying an NBC protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         iron-nitrosyl hemoglobin; electron paramagnetic resonance; UV spectra; PFR; nitric oxide; antianemic; antibacterial; immunosuppressive; vasotropic; antiinflammatory; antiasthmatic; respiratory; antiarthritic; cerebroprotective; red blood cell membrane defect; vasculopathy; septic shook mycoardial depression; panoreatitis; sickle cell crisis; urinary tract infection; progressive respiratory failure; septicemia; ischemia; arthritis; asthma; cerebritis; bronchitis; vasculitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel method for determining the predominant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Determining predominant physiological effect of composition comprising hemoglobin used to produce methods of therapy for medical disorders by using EPR or UV spectra of iron nitrosyl hemoglobin derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Erythrocyte band 3 anion transporter protein; human; hypercoagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human erythrocyte band 3 anion transporter protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 104; DB 20; 100.0%; Pred. No. 2.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB46914 standard; protein; 911 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 11; 70pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             720 GMPWLSATTVRSVTHANALT 739
Example 1; Fig 5; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Singel DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-AUG-2000; 2000WO-US21101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYDU-) UNIV DUKE.
(RERE-) RES & DEV INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GOW AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-183002/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200109616-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stamler JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-FEB-2001
```

ô

```
.
0
                                                                 intic contact (NO) with menugations and accommission to the composition of the composition of the composition of the products of the invention have antianemic; antibacterial; immunosuppressive; vasotropic; antiantiantanto; antiantianemic; antianthmatic; respiratory; antiarthritic and cerebroprotective activity. The products of the invention are used to produce methods of therapy for medical disorders characterized by red blood cell membrane defects and for a variety of hypercoagulable and vasculopathic states, particularly for patients with septic shock who develop myocardial depression, perintitis and progressive respiratory failure, patients with septicemia as a complication of urinary tract infection and patients with ischemia, patients in a sickle cell crisis and for treating inflammatory
                 involves obtaining electron paramagnetic resonance (EPR) or UV spectra of iron-nitrosyl hemoglobin derivatives formed by incubation of limiting nitric oxide (NO) with hemoglobin and determining if the composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptide; malarial infection; drug resistance; vaccine; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated Band 3 polypeptide that comprises any of 4 20 residue amino acid sequences, or their fragments that bind to an MSP-1 polypeptide or a polypeptide with any of 8 291-1331 base pair sequences. The methods and compositions of the present invention are useful for the prevention and treatment of malarial infection. The present invention, develops new and more improved methods based upon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Band 3 polypeptide which selectively binds to merozite surface protein-1, useful for the prevention and treatment of malarial infection
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                conditions such as arthritis, asthma, cerebritis, bronchitis and vasculitis. The methods are also used for preserving red blood cells
physiological effect of a composition comprising hemoglobin which
                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                     Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 104; DB 22; 100.0%; Pred. No. 2.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 102–105; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SELI-) ST ELIZABETH'S MEDICAL CENT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goel V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE29343 standard; Protein; 911 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    720 GMPWLSATTVRSVTHANALT 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GMPWLSATTVRSVTHANALT. 20
                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                        which can be used in therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002; 2002WO-US06415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-MAR-2001; 2001US-272930P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
nes 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Band 3 protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chishti AH, Oh SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI 34,2002-759814/82.
N-PSDB; AAD46978.
                                                                                                                                                                                                                                                                                                                                                             911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200270542-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; Band 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protozoacide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE29343;
                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE29343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

inhibiting the particular interactions between the malarial parasite and

```
ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
a cognate molecule present in the host and subsequently minimising harmful side effects and drug resistance that may be due to non-specific therapeutic approaches. The invention is useful in gene therapy. The present invention also provides a vaccine for malaria. The present sequence is human Band 3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated Band 3 polypeptide that comprises any of 4 20 residue amino acid sequences, or their fragments that bind to an MSP-1 polypeptide or a polypeptide with any of 8 291-131 base pair sequences. The methods and compositions of the present invention are useful for the prevention and treatment of malarial infection. The present invention, develops new and more improved methods based upon inhibiting the particular interactions between the malarial parasite and a cognate molecule present in the host and subsequently minimising harmful side effects and drug resistance that may be due to non-specific threapeutic approaches. The invention is useful in gene therapy. The present invention also provides a vaccine for malaria. The present sequence is human Band 3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                              malarial infection; drug resistance; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated Band 3 polypeptide which selectively binds to merozite surface protein-1, useful for the prevention and treatment of malarial infection -
                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                ;
                                                                                                                                  911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 911;
                                                                                                                                  Length
                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 104; DB 23;
Pred. No. 2.1e-08;
Mismatches 0;
                                                                                                                                Score 104; DB 23;
Pred. No. 2.1e-08;
                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 107-110; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SELI-) ST ELIZABETH'S MEDICAL CENT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goel V;
                                                                                                                                                                                                                                                                                                               AAE29344 standard; Protein; 911 AA.
                                                                                                                                                                                                                  720 GMPWLSATTVRSVTHANALT 739
                                                                                                                                                                                                 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                ;
0
                                                                                                                               100.0%;
                                                                                                                                                                                                 1 GMPWLSATTVRSVTHANALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%;
Best Local Similarity 100.0%;
Matches 20; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002; 2002WO-US06415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAR-2001; 2001US-272930P
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; Band 3 polypeptide;
protozoacide; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                         Query Match
Best Local Similarity 100.7
Matches 20, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               Human Band 3 protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oh ss,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-759814/82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        911 AA;
                                                                                                  911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAD46979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200270542-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chishti AH,
                                                                                                                                                                                                                                                                                                                                                                               27-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-SEP-2002
                                                                                                                                                                                                                                                                                                                                                 AAE29344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ношо
                                                                                                                                                                                                                                                                                  RESULT 14
                                                                                                                                                                                                                                                                                                   AAE29344
                                                                                                                                                                                                                                                                                                                                                                               ò
   8
                                                                                                                                                                                                                               qq
```

```
The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying at the appendic of pathology related to aberrant expression or physiological interactions of the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. They may be used to the rappy, and can be useful in genetic vaccination, testing and the rappy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopolesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU2510-AAU3304 represent the amino acid sequences of novel human secreted proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 104; DB 22; 100.0%; Pred. No. 2.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; Page 354; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human secreted protein #1316.
                                                                                                                                                                                                                                      AAU30825 standard; Protein; 962 AA
720 GMPWLSATTVRSVTHANALT 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-APR-2000; 2000US-0552929.
26-JAN-2001; 2001US-0770160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-APR-2001; 2001WO-US08656.
                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.(
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-611725/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              962 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tang YT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200179449-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                             18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-OCT-2001.
                                                                                                                                                                                                                                                                                                               AAU30825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                RESULT 15
                                                                                                                                                                                                         AAU30825
                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME OF THE OF T
```

; 0

Gaps

ö

Indels

; 0

0; Mismatches

Search completed: September 3, 2003, 11:46:11 Job time: 50.5 secs

771 GMPWLSATTVRSVTHANALT 790

1 GMPWLSATTVRSVTHANALT 20

οy g

```
Q8by17 mus musculu Q8by17 mus musculu Q9kk43 homo sapien Q9kkb6 setrakhan r Q9kka4 rickettsia Q9kka7 rickettsia Q9kkb8 rickettsia Q9kkb8 rickettsia Q9kkb8 musculu
                                                                                                                                                                     O8gzwl oryza sativ
Q92vy7 rhizobium m
O95233 homo sapien
                                                                                                                                                                                                                                    sapien
musculu
                                                                                                                                                                                                                  OBcfs3 mus musculu
O9hcq6 homo sapien
                             Q9erp5 mus musculu
Q99416 homo sapien
Q13717 homo sapien
Q95sw2 drosophila
Q8mrk3 drosophila
Q8iqd4 drosophila
Q8iqd6 drosophila
Q8iqd5 drosophila
Q9vt48 drosophila
                                                                                                                                                                                                                                                                                mus musculu
mus musculu
   brachydanio
                                                                                                                                                                                                                                                                    mus musculu
                                                homo sapien
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E SEQUENCE A.C.

(A TISSUE-Colon;

RT "Molecular cloning and characterization of band 3 anion exchange
RT protein (AEI) mRNA from rat colon.";

RD britted (APR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY030082; AAX38733.1; -.

DR InterPro; IPR001717; Anion.exchange.

InterPro; IPR001717; Anion.exchange.

PRINTS; PR01231; HCO3_cotranspt.

PRINTS; PR01231; HCO3_cotranspt.

PRINTS; PR01231; HCO3TRNSPORT.

DR TIGREMAS; TIGR00834; ae: 1.

DR PROSTIE: PS00219; ANION_EXCHANGER_1; 1.

PROSTIE: PS00219; ANION_EXCHANGER_2; 1.

SFOUENCE 849 AA: 94312 MW; E4BZ00780CB07D3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                 Q9est0 mus m
Q8c943 mus m
Q9jkv6 mus m
Q8jzr6 mus m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92.9%; Score 91; DB 11; Length 849; 95.0%; Pred. No. 3.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DRC-2003 (TrEMBLrel. 23, Last annotation update)
Band 3 anton exchange protein.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  849 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                           013717
0855W2
08055W2
0810D6
0810D6
0810D5
091074
0952W1
0952W3
0952W3
0952W3
0952W3
0952W3
0953W3
0958W4
098W4
098W4
098W4
098W4
098W4
098W4
098W4
098W4
Q8JFT9
Q9ERP4
Q9ERP5
                                                                                                                                                                                                                                                                                                                                                                                                        Q9KKA7
                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8BWZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVTHANALTVMGKASGPGAA 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SVTHANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                             1614
1615
1616
1616
1616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
NCBI_TaxID=10116;
61
61
61
61
57
57
51
51
51
51
64
47.5
                                                                                                                                                                                                                    699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 1
 711188
711188
711188
711188
711188
711188
711188
711188
711188
711188
711188
711188
711188
711188
711188
711188
711188
711188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0912E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A PACCOCC OCT A PACCOCC A PACCOCCA A PACCOCCA PACCOCCA PACCOCCA PACCOCCA PACCOCCA A PACCOCCA PACCOCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9tu75 sus scrofa
Q8tag3 homo sapien
Q90710 gallus gall
Q9uey4 homo sapien
Q9uey5 homo sapien
Q99654 homo sapien
Q9uey6 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q91ze7 rattus norv
19tuq0 bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oguey6 homo sapien
P79877 lampetra ja
O90579 gallus gall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9udjl homo sapien
Q91452 oncorhynchu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              035225 cynomys lud
Q991t5 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9xsw5 bos taurus
                                                                                                       3, 2003, 11:40:18; Search time 44.5 Seconds (without alignments) 115.979 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9tuq0
                                                                                                                                                                                                                                                                                                               830525
              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                            OM protein - protein search, using sw model
                                                                                                                                                                   US-10-087-464-2
98
1 SVTHANALIVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8TAG3
Q90710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        099654
09UEY6
P79877
090579
09UDJ1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q91ZE7
Q9TUQ0
Q9XSW5
Q35225
Q99LT5
                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9UEY4
Q9UEY5
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPTREMBL_23:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 4 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_rodent:*
sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_mammal:*
sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            622
1159
12159
1219
1227
1241
1241
160
844
124
124
160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               466
                                                                                                          September
                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91
73
73
73
73
73
73
64
67
67
63
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                       Sequence:
                                                                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š.
```

```
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               035225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    099LT5;
                                                                                                                                                                                                                                                                                                                                                                                                                                      035225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q99LT5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLC4A2
                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
035225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
Q99LT5
                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQ
                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Koshino I. Inaba M., Matsumoto M., Ono K.;
"Band 3 gene associated
"Band 3 Bov Nippon: a nonsense mutation in the band 3 gene associated
with decreased mutant mRNA possessing dominant negative effect and
dominant hereditary spherocytosis in cattle.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
BMBL; AF163028; AAD43354.1;
"InterPro: IPR003107; Anion_exchange.
InterPro: IPR003107; Anion_exchange.
InterPro: IPR003205; HCO3_cotranspt.
Pfam; PF00555; HCO3_cotranspt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Bone marrow;

Koshino I., Inaba M., Matsumoto M., Ono K.;

Koshino I., Inaba M., Matsumoto M., Ono K.;

"Band 3 Bov. Nippon: a nonsense mutation in the band 3 gene associated with decreased mutant mRNA possessing dominant negative effect and dominant hereditary spherocytosis in cattle.";

Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF163826; AAD43593.1;

EMBL; AF163826; AAD43593.1;

InterPro; IPR001717; Anion_exchange.

InterPro; IPR001717; Anion_exchange.

InterPro; IPR0032cotranspt.

Pfam; PF00955; HCO3_cotranspt.

Pfam; PF00955; HCO3_cotranspt.

Pfam; PR001231; HCO3_cotranspt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
NCBI_TaxID-9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.6%; Score 79; DB 6; Length 855;
84.2%; Pred. No. 0.00034;
.ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
GEQUENCE 930 Aa; 104374 MM; 4F6AADFEBAF6A3A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SEQUENCE 855 AA; 95643 MW; 06CD037324F69872 CRC64;
                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                         855 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          930 AA.
                                                                                                                Created)
                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SVTHANALTVMGKASTPGA 19
                                                                                                    01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2003 (TrEMBLrel. 23, Band 3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2003 (TrEMBLrel. 23, Band 3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGREAMS; TIGRO0834; ae; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 84.2*
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FIGREAMS; TIGRO0834; ae;
                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Kidney
                                     O9TUO0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O9XSW5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
Q9XSW5
Q9TUQ0
                                         DDT REPORT OF THE PROPERTY OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A PAC O O C O O C O O C O O C O O C O O C O O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O C O
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          Cynomys ludovicianus (Black-tailed prairie dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Abedin 2.R., Moser A.J., Roslyn J.J., Abedin M.Z.; "Expression of anion exchange protein 2 (AE-2) in gallbladder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 73; DB 11; Length 103;
         Length 930;
                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           epithelia.";
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF012895; AAB66833.1;
InterPro; IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotransp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002234; AAH02234.1; -
MGD; MGI:109351; S1c4a2.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HG03_cotranspt.
Pfan; PF00955; HG03_cotranspt.
PRINTS; PR01231; HG03TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 AA; 11012 MW; 29A99247E768B455 CRC64;
                                                                                                                                                                                                                                                                                                         01-0AN-1998 (TrEMBLrel. 05, Created)
01-0AN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Hypothetical 52.0 kDa protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 0.00035;
cches 3;
         Score 79; DB 6; Pred. No. 0.00037;
                                                                                                                                                                                                                                                                     103 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    466 AA
                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 0.00
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGRFAMs; TIGRO0834; ae; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                 Anion exchange protein 2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                           1 SVTHANALTVMGKASTPGA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 SVTHANALTVMSKAVAPG 72
         80.6%;
84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match · · 74.5
Best Local Similarity 83.3
Matches 15; Conservative
                                                       Conservative
                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=Gall bladder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=45480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103
```

FT

ò 셤

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE-96224107; PubMed-8621532;

Cox K.H., Adair-Kirk T.L., Cox J.V.;

Cox K.H., Adair-Kirk T.L., Cox J.V.;

'variant AEZ anion exchanger transcripts accumulate in multiple cell

types in the chicken gastric epithelium.";

J. Biol. Chem. 271:8895-8902(1996).

EMBL; U48899; AAC59881.1; -.

HSSP; P02730; 1BTQ.
                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1219;
                                                                                                                                                                                                                                                                                            74.5%; Score 73; DB 4; Length 1159; 83.3%; Pred. No. 0.0044;
     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                 TIGRFAMS; TIGRO0834; ae; 1.
PROSTIE; PS00219; ANION_EXCHANGER_1; 1.
PROSTIE; PS00220; ANION_EXCHANGER_2; 1.
SEQUENCE 1159 AA: 127747 WW; 9F083A2BE8FF5D74 CRC64;
                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGRFAMS; TIGRO0834; ae; 1.
PROSTIE; PS00219; ANITON_EXCHANGER_1; 1.
PROSTIE; PS00220; ANITON_EXCHANGER_2; 1.
SEQUENCE 1219 AA; 135288 MW; 25F42A73C3483B21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                         Strausberg R.; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC028601; AAH28601.1; InterPro: IPR001717; Anion_exchange. InterPro: IPR003020; HC03_cotranspt. PF00955; HC03_cotranspt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9UEY4 PRELIMINARY; PRT; 1227 AA. 09UEY4; 01TEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 73; DB 13;
Pred. No. 0.0047;
0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1219 AA.
                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HGO3_cotranspt.
Pfam; PF00955; HGO3_cotranspt.
PRINTS; PR01231; HGO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1040 SVTHANALTVMSKAVAPG 1057
                                                                                                                                                                                                                                                                                                                                                                                       979 SVTHANALTVMSKAVAPG 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18
                                                                                                                                                                                                                                                                                                                                                                  1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.5%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 01, (TrEMBLrel. 01, (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SVTHANALTVMGKASTPG
                                                                                                                                                                                                                                                                                            Query Match 74.5
Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AE2.
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AE2-1 anion exchanger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=Proventriculus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 15; Conserv
                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9031;
                    NCBI_TaxID=9606;
                                                                             TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             090710
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
Q90710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9UEY4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ID
DT
DT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   엄
   ò
                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zolotarev A.S., Chernova M.N., Yannoukakos D., Alper S.L.;
Proteolytic cleavage sites of native AE2 anion exchanger in gastric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Stomach,

PISSUE-Stomach,

BDLINE-99315230; PubMed-10387099;

Zolotarev A.S., Shmukler B.E., Alper S.L.;

"AEZ anion excipanger polypeptide is a homooligomer in pig gastric membranes: a chemical cross-linking study.";

Bothemistry 38.8521-8531(1999).

EMBL; AF120099; AAF00977.1; -.

HSSP; P02730; 1BTQ.
                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to solute carrier family 4, anion exchanger, member 2
(Erythrocyte membrane protein band 3-like 1).
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                               Score 73; DB 11; Length 466;
Pred. No. 0.0017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 73; DB 6; Length 622,
Pred. No. 0.0023;
0; Mismatches 3; Indels
       1
52003 MW; 481C1108E28D03B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68713 MW; 58B013462C36E1DC CRC64;
                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Chloride-bicarbonate anion exchanger AE2 (Fragment)
                                       74.5%; Scor.
83.3%; Pred. No. v..
0; Mismatches
                                                                                                                                                                                                                                                          622 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1159 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGRRAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HC03_cotranspt.
Pfam; PF00955; HC03_cotranspt.
PRINTS; PR01231; HC03TRNSPORT.
                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Stomach;
MEDLINE=96339307; PubMed=8756692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochemistry 35:10367-10376(1996)
                                                                                                                                               1111111111 | 1 | 1 | 286 SVTHANALTVMSKAVAPG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVTHANALTVMSKAVAPG 459
                                                                                                                             1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 74.5%;
Local Similarity 83.3%;
nes 15; Conservative (
                                                     Query Match
Best Local Similarity 83.33
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                        PRELIMINARY;
                 466 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mucosal membranes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         622 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9823;
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8TAG3;
                                                                                                                                                                                                                                                      Q9TU75
Q9TU75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8TAG3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                      RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8TAG3
```

ö

ŏ g OS DE DIT

```
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
'-hac 15; Conserva
                                                                                                                                                                                                                                                                   AE2 anion exchanger.
SLC4A2.
 HSSP; P02730; 1BTO.
                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                     Query Match
                                                                                                                                                                                                                             299654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9UEY6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLC4A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9UEY6
                                                                                                                                                                                                                  099654
                                                                                                                                                                                               RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09UEY6
 g
                                                                                                                                              ò
                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                       Gaps
                             Homo sapiens (Human).
businaryara Mentara Mentara Mentebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                       Medina J.F., Lecanda J., Acin A., Clesielczyk P., Prieto J.;
"Tissue-specific N-terminal isoforms from overlapping alternate promoters of the human AE2 anion exchanger gene.";
Biochem. Biophys. Res. Commun. 267:228-235(2000).
EMBL; U76669; AAF19584.2;
EMBL; U76669; AAF19584.2;
HSSP; P02730; 1BTQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDIJNE=97179202; PubMed=9027488;
Medina J.F., Acin A., Prieto J.;
Molecular cloning and characterization of the human AE2 anion exchanger (SLC4A2) gene.";
Genomics 39:74-85(1997).
                                                                             SEQUENCE FROM N.A.
MEDLINE=97179202; PubMed=9027488;
Medina J.F., Acin A., Prieto J.;
"Molecular cloning and characterization of the human AE2 anion exchanger (SLC4A2) gene.";
Genomics 39:74-85(1997).
                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                 74.5%; Score 73; DB 4; Length 1227; 83.3%; Pred. No. 0.0047; 1ve 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                       PRINTS; FRULLOWS AS 1.

PROSTER PROSTE; TIGRO0834; ARION_EXCHANGER_1; 1.

PROSITE; PS00220; ANION_EXCHANGER_2; 1.

PROSITE; PS00220; ANION_EXCHANGER_2; 1.

PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1232 AA.
                                                                                                                                                                                                                                                        InterPro; IPR001717; Anion_exchange.
InterPro; IPR003005; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotranspt.
PRINTS; PR01231; HCO37RNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                    1047 SVTHANALTVMSKAVAPG 1064
                                                                                                                                                                                                                                                                                                                                                                                         1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2003 (TrEMBLrel. 23, Anion exchanger 2 type b2.
                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 83.3
Matches 15; Conservative
         exchanger 2 type bl
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20090621;
                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9UEY5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9UEY5
                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9UEY5
g
                                                                                                                                                                                                                                                                                                                                                                                           ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE-97179202; PubMed-9027488;

Medina J.F., Acin A., Prieto J.;

Molecular cloning and characterization of the human AE2 anion exchanger (SLC4A2) gene.";

Genomics 39:74-85(1997).

EMBL; U62531; AAC50964.1; -.

HSSP; P02730; 1BPQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1241;
                                                                                                                                                                                                                                 Length 1232;
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
InterPro; PR00350; HCO3_cotranspt.
PR01031; HCO3_cotransp; 1.
PR01731; HCO3TRNSPORT.
IIGRFAMS; TIGR00834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SEQUENCE 1232 AA; 136218 MW; 22688C662907C2D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGRFAMS; TIGR00834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SEQUENCE 131019 WW; D266ECDAB238FD97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Anion exchanger 2 type a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.5%; Score 73; DB 4; Let
83.3%; Pred. No. 0.0047;
                                                                                                                                                                                                                                 Score 73; DB 4;
Pred. No. 0.0047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1241 AA
                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HC03_cctranspt.
Pfam: PF00955; HC03_cctranspt.
PRINTS; PR01231; HC03TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                 1052 SVTHANALTVMSKAVAPG 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1061 SVTHANALTVMSKAVAPG 1078
                                                                                                                                                                                                                                                                                                                                       1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                 74.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1997 (TrEMBLrel. 03, 01-MAY-1997 (TrEMBLrel. 03, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                           Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
```

```
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kang D., Okubo K., Hamasaki N., Kuroda N., Shiraki H.,
"A structural study of the membrane domain of band 3 by tryptic
digestion. Conformational change of band 3 in situ induced by alkali
treatment.":
J. Biol. Chem. 267:19211-19217(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                     Cox J.V., Lazarides E.;
"Alternative primary structures in the transmembrane domain of the chicken erythroid anion transporter.";
Mol. Cell. Biol. 8:1327-1335(1988).
EMBL; M19496; AAA48604.1; --
HSSP; P02730; 1BTQ.
InterPro; IPR001177; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfam; PF0055; HCO3_cotranspt.
Pfam; PF0055; HCO3_cotranspt.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9UDJ1;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Band 3 protein (Fragments).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 68.4%; Score 67; DB 4; Length 124; Best Local Similarity 93.3%; Pred. No. 0.0041; Matches 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00119; ANION EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SEQUENCE 844 AA; 93808 MW; C463F993D5974276 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13001 MW; E2028D64A8E4A4D1 CRC64;
    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 71; DB 13;
Pred. No. 0.0067;
5; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92406862; PubMed=1527044;
                                                                                                                                                                                                                      MEDLINE=88216609; PubMed=2835670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.4%;
66.7%;
                                                             Erythroid anion transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SVTHANALTVMGKAS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGREAMS; TIGRO0834; ae; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.73
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                             NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_CONS
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_CONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_CONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON CONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_CONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_CONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
                                                                                                                                           Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9UDJ1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
Q9UDJ1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kay M.M., Cover C., Schluter S.F., Bernstein R.M., Marchalonis J.J.;
"Band 3, the anion transporter, is conserved during evolution:
implications for aging and vertebrate evolution.";
Cell. Mol. Biol. 41:833-842(1995).
EMBL, S80168; AAD14330.1;
InterPro; IPR003020; HC03_cotranspt.
Pfam, PF00955; HC03_cotranspt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lampetra japonica (Japanese lamprey) (Entosphenus japonicus).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Pertomyzontiformes; Petromyzontidae; Lethenteron.
NCBI_TaxID-94989;
                                                                                                                                                                           Medina J.F., Lecanda J., Acin A., Clesielczyk P., Prieto J.; "Tissue-specific N-terminal isoforms from overlapping alternate promoters of the human AE2 anion exchanger gene."; Biochem. Biochem. Esophys. Res. Commun. 267:228-235(2000).
SEQUENCE FROM N.A. MEDLINE-97179202; PubMed-9027488; Medina J.F., Acin A., Prieto J.; Madina J.F., Acin A., Prieto J.; "Molecular cloning and characterization of the human AE2 anion exchanger (SLC4A2) gene."; Genomics 39:74-85(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 73; DB 4; Length 1241;
Pred. No. 0.0047;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 73.5%; Score 72; DB 13; Length 160; Best Local Similarity 77.8%; Pred. No. 0.00081; Matches 14; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HC03_cotranspt.
Pfam; PF00955; HC03_cotranspt.
PROWIPS; HC0311; HC03_TRNSPORT.
TIGRRAMS; TIGR00834; ae; 1.
TIGRRAMS; TIGR00834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
SEQUENCE 1241 AA; 136980 MW; D2FDA72E20D70D64 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160 AA; 17329 MW; A5EE8C029518A2B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P79877;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Major anion transport protein band 3 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 844 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                       Biochem. Biophys. Res. Commun. 267
EMBL; U76669; ART19583.2; -.
EMBL; U76667; AAF19583.2; JOINED.
EMBL; U76668; AAF19583.2; JOINED.
HSSP; P02730; 1BTQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96089372; PubMed=8535177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1061 SVTHANALTVMSKAVAPG 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVTHVNALTVMSKATAPG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 74.5%;
Best Local Similarity 83.3%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                      [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                             MEDLINE-20090621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
Q90579
ID Q90579
AC Q90579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P79877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
```

P79877

οy a

ò g

ö

g

Search completed: September 3, 2003, 11:50:03 Job time : 46.5 secs

```
SEQ ID NO 2
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10954, A
Sequence 2, Appli
Sequence 4, Appli
Sequence 8, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Appli
Sequence 22, Appl
Sequence 39328, A
Sequence 6, Appli
Sequence 6, Appli
                                                                                                                                                                                                                                                                              September 3, 2003, 11:46:23 ; Search time 17.5 Seconds
(without alignments)
156.918 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / (gn2_6/ptodata//pubpaa/US07_PUBCOMB.ppp:*
/ (gn2_6/ptodata//pubpaa/US07_NEW_PUB.ppp:*
/ (gn2_6/ptodata//pubpaa/US06_NEW_PUB.ppp:*
/ (gn2_6/ptodata//pubpaa/US06_PUBCOMB.ppp:*
/ (gn2_6/ptodata//pubpaa/US07_NEW_PUB.ppp:*
/ (gn2_6/ptodata//pubpaa/PCUG2_PUBCOMB.ppp:*
/ (gn2_6/ptodata//pubpaa/US08_NEW_PUB.ppp:*
/ (gn2_6/ptodata//pubpaa/US08_PUBCOMB.ppp:*
/ (gn2_6/ptodata//pubpaa/US08_PUBCOMB.ppp:*
/ (gn2_6/ptodata//pubpaa/US08_PUBCOMB.ppp:*
/ (gn2_6/ptodata//pubpaa/US09_PUBCOMB.ppp:*
/ (gn2_6/ptodata//pubpaa/US09_PUBCOMB.ppp:*
/ (gn2_6/ptodata//pubpaa/US09_PUBCOMB.ppp:*
/ (gn2_6/ptodata//pubpaa/US09_PUBCOMB.ppp:*
/ (gn2_6/ptodata//pubpaa/US09_PUBCOMB.ppp:*
/ (gn2_6/ptodata//pubpaa/US09_PUBCOMB.ppp:*
/ (gn2_6/ptodata//pubpaa/US10A_PUBCOMB.ppp:*
/ (gn2_6/ptodata//pubpaa/US10A_PUBCOMB.ppp:*
/ (gn2_6/ptodata//pubpaa/US10A_PUBCOMB.ppp:*
/ (gn2_6/ptodata//pubpaa/US10A_PUBCOMB.ppp:*
/ (gn2_6/ptodata//pubpaa/US10A_PUBCOMB.ppp:*
/ (gn2_6/ptodata//pubpaa/US10A_PUB.ppp:*
/ (gn2_6/ptodata///pubpaa/US10A_PUB.ppp:*
/ (gn2_6/ptodata///pubpaa/US10A_PUB.ppp:*
/ (gn2_6/ptodata///pubpaa/US10A_PUB.ppp:*
/ (gn2_6/ptodata///pubpaa/US10A_PUB.ppp:*
/ (gn2_6/ptodata///pubpaa/US10A_PUB.ppp:*
/ (gn2_6/ptodata///pubpaa/US10A_PUB.puB.pp:*
/ (gn2_6/ptodata///pubpaa/US10A_PUB.puB.pp:*
/ (gn2_6/ptodata///pubpaa/US10A_PUB.puB.pp:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 US-10-087-464-2

US-10-087-464-22

US-10-0864-761-39328

US-10-086-320-2

US-10-087-464-8

US-10-087-464-8

US-09-15-242-10954

US-09-728-137-4

US-09-728-137-4

US-09-728-137-2

US-09-728-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       513375 seqs, 137303645 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                             - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SVTHANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table: 'BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-087-464-2
98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               911
911
262
262
714
714
1032
1085
1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     998
998
998
998
774
777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB
Maximum DB
                                                                                                                                                                                        OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sedneuce:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database
                                                                                                                                                                                                                                                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
```

```
        16
        47
        48.0
        1129
        9
        US-09-734-674-2
        Sequence 2, Appli

        17
        46
        48.0
        1129
        15
        US-10-274-990-2
        Sequence 2, Appli

        19
        45
        45.9
        20
        15
        US-10-087-464-3
        Sequence 1, Appli

        20
        44
        44.9
        27
        10
        US-10-087-464-1
        Sequence 1, Appli

        21
        44
        44.9
        27
        10
        US-09-925-300-1450
        Sequence 1, Appli

        22
        43
        9
        526
        9
        US-09-925-300-1450
        Sequence 1, Appli

        23
        42.9
        4551
        11
        US-09-986-384-3
        Sequence 1, Appli

        24
        42.9
        4551
        12
        US-10-216-39-1
        Sequence 1, Appli

        25
        42.9
        4613
        10
        US-09-884-8848-3
        Sequence 1, Appli

        26
        42.9
        4613
        11
        US-09-886-8848-3
        Sequence 1, Appli

        27
        42.9
        4613
        11
        US-09-886-8848-3
        Sequence 1, Appli

        28
        42.9</
```

ALIGNMEN

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                            INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
INFORMATION: EXPRESSED IN BOULT LIVER, SIGNAL = 1.5
INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
INFORMATION: SWISSPROT HIT: PO2730, EVALUE 3.00e-31
INFORMATION: EXPLAINT: BEF26005.1, EVALUE 3.00e-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 98; DB 9; Length 86;
Pred. No. 6.4e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Standary, Jonathan S.
APPLICANT: Standary, Jonathan S.
APPLICANT: Standary, Javid J.
APPLICANT: Singel, David J.
TITLE OF INVENTION: Method for Determining Physiological
TITLE OF INVENTION: Effects of Hemoglobin
FILLE REFERENCE: 1818, 1030-003
CURRENT APPLICATION NUMBER: US/10/066, 320
CURRENT FILING DATE: 2002-01-31
PRIOR FILING DATE: 2002-01-31
PRIOR PLILOR DATE: 2000-08-02
PRIOR FILING DATE: 1999-08-02
PRIOR FILING DATE: 1999-08-02
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
      PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 39328
LENGTH: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 98; DB 15;
Pred. No. 9.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/10066320 Publication No. US20030022267A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SVTHANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/10087464 Publication No. US20030059436A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 SVTHANALTVMGKASTPGAA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SVTHANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100...
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Chishti, Athar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 1
                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                           OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                     INFORMATION:
INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-864-761-39328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-066-320-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                 OTHER
OTHER
OTHER
OTHER
                                                                                                                                                                                                                                                                               OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                          APPLICANT: Goel, Vikas
APPLICANT: Li, Xuerong
TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
FILE REFERENCE: S1337/7019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                        Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 98; DB 15; Best Local Similarity 100.0%; Pred. No. 2.8e-09; Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                            red. No. 2.8e-09;
Mismatches 0;
                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/087,464
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 06/272,930
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.0
LENGTH: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/USO1/00670
PTITING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US01/00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2001-01-30
APPLICATION NUMBER: PCI/US01/00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 09/532,366
APPLICATION NUMBER: US 09/632,366
FILING DATE: 2000-08-03
PULICATION NUMBER: GB 24263.6
FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 39328, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SVTHANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVTHANALTVMGKASTPGAA 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-01-30
Chishti, Athar
                                      Liu, David
                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapien
                 Steven
                                                                                                                                                                                                                                                                                                                                                                US-10-087-464-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR
PRIOR
PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a.
```

```
Sequence 2, Application US/10260877

Sequence 2, Application WS/10260877

Bublication No. US20030021813A1

GENERAL INFORMATION:
APPLICANT: Abbort Laboratories

APPLICANT: Chovan, Linda E.
APPLICANT: Reich, Karl A.
TITLE OF INVENTION: ESCENTIAL BACTERIA GENES AND GENOME
TITLE OF INVENTION: CASSENTIAL GENES'
TITLE OF INVENTION: CASSENTIAL GENES'
TITLE OF INVENTION: WINDER: US/10/260,877

CURRENT APPLICATION NUMBER: US/10/260,877

CURRENT FILING DATE: 2002-09-30

PRIOR FILING DATE: 2000-08-25

NUMBER OF SEQ ID NOS: 137

SOFTWARE: RestSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokarvotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 49; DB 1
Pred. No. 3.2;
4; Mismatches
                              TILLE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILIDE DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-26
PRIOR PLICATION NUMBER: 60/207,727
PRIOR PLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF ESQ 1D NOS: 14110
SEQ 1D NO 10954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-728-137-4
; Sequence 4, Application US/09728137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :||| | || |::| |::|
175 SHANFLEVMHKSATKGSA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-815-242-10954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :||| | || |::| |:|
175 SHANFLEVMHKSATKGSA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 THANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 THANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.0%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 55.6'
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 50.0
Best Local Similarity 55.6
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: H. influenzae
US-10-260-877-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 2
LENGTH: 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Chishli, Athar
APPLICANT: Oh, Steven
APPLICANT: Liu, David
APPLICANTON: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
FILE REFERENCE: S1237/7019
CURRENT APPLICATION NUMBER: US 10/02-03-01
PRIOR APPLICATION NUMBER: US 06/272,930
PROFUN FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.0
SEQ ID NO 8
LENGTH: 911
              APPLICANT: Liu, David
APPLICANT: Gool, Vikas
APPLICANT: Gool, Vikas
APPLICANT: Gool, Vikas
APPLICANT: Gool, Vikas
APPLICANT: Li, Xuerong
TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
CURRENT APPLICATION NUMBER: US/10/087,464
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 06/272,930
PRIOR APPLICATION NOWBER: US 06/272,930
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                              Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 98; DB 15;
Pred. No. 9.7e-08;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                         Score 98; DB 15;
Pred. No. 9.7e-08;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10954, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             731 SVTHANALTVMGKASTPGAA 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SVTHANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SVTHANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/10087464 Publication No. US20030059436Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Some Best Local Similarity 100.0%; P. Matches 20; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 20; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari T
                                                                                                                                                                                                                                                                                                                                  ); ORGANISM: Homo sapiens
US-10-087-464-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Oh, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-815-242-10954
                                                                                                                                                                                                                                                               SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-087-464-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Hc
US-10-087-464-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

```
Sequence 4, Application US/09734674
Pettent No. US20020081648A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLOOlol8
CURRENT FILING NUMBER: US/09/734,674
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:|| |:| : | ||
850 SITHVNSLKLESECSAPG 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SVTHANALTVMGKASTPG 18
Query Match 48.0%;
Best Local Similarity 44.4%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 44.4v
Local Similarity 44.4v
Local Similarity 44.4v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 4
LENGTH: 1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS-09-728-137-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                            Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47; DB 9; Length 714;
Pred. No. 22;
4; Mismatches 6; Indels
                                                                     APPLICANT: AUTOLINE ACTION APPLICANT: AVIET MATCH APPLICANT: Xavier Martin APPLICANT: Xavier Martin APPLICANT: Xavier Martin APPLICANT: Steven Charles Jupe APPLICANT: Christopher John Rawlings APPLICANT: Trudy Rachel Doe TITLE OF INVENTION: NOVEL COMPOUNDS FILE REFERENCE: GH-30409-D1 CURRENT FILING DATE: 2000-12-01 PRIOR APPLICATION NUMBER: US/9/728,137 CURRENT FILING DATE: 1998-07-15 PRIOR PELICATION NUMBER: EP 97401714.7 PRIOR FILING DATE: 1997-07-16 PRIOR FILING DATE: 1997-07-16 PRIOR FILING DATE: 1997-07-16 PRIOR FILING DATE: 1998-02-09 PRIOR FILING DATE: 1998-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Xavier Martin
APPLICANT: Xavier Martin
APPLICANT: Steven Charles Jupe
APPLICANT: Steven Charles Jupe
APPLICANT: Trudy Rachel Don Rawlings
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30409-D1
CURRENT APPLICATION NUMBER: US/09/728,137
CURRENT FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: EP 97401714.7
PRIOR PELING DATE: 1997-07-16
PRIOR APPLICATION NUMBER: EP 97401714.7
PRIOR PELING DATE: 1997-07-16
PRIOR PELING DATE: 1997-07-16
PRIOR PELING DATE: 1998-02-09
PRIOR PELING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: EP 98400454.9
PRIOR PELING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: EP 98400454.9
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: EP 98400454.9
PRIOR FILING DATE: 1998-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NOS: 10
FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Walter F. Boron
Antoine Michel Alain Bril
Nassirah Khandoudi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/09728137
Patent No. US20010029031A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:|| |:| : | ||
520 SITHVNSLKLESECSAPG 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 44.4%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: HOMO SAPIENS
dS_09-728-137-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: HOMO SAPIENS
US-09-728-137-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 4
LENGTH: 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID'NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
```

```
ö
                                               Gaps
                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
  Length 1032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1044;
core 47; DB 9;
ed. No. 34;
Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 9;
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Xavier Martin
APPLICANT: Steven Charles Jupe
APPLICANT: Steven Charles Jupe
APPLICANT: Steven Charles Jupe
APPLICANT: Steven Charles Jupe
APPLICANT: Trudy Rachel Doe
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REPERENCE: GH-30409-D1
CURRENT APPLICATION NUMBER: US/97728,137
CURRENT FILING DATE: 1996-07-15
PRIOR PRIOR APPLICATION NUMBER: EP 97401714.7
PRIOR FILING DATE: 1997-07-16
PRIOR FILING DATE: 1997-07-16
PRIOR FILING DATE: 1997-07-16
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: EP 98400272.5
PRIOR FILING DATE: 1998-02-09
PRIOR FILING DATE: 1998-02-09
PRIOR FILING DATE: 1998-02-05
NUMBER: PSEQ ID NOS: 10
SEQ ID NO 2
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 47; DB Pred. No. 34;
  Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                           Antoine Michel Alain Bril
Nassirah Khandoudi
                                                                                                                                                                                                                                                      Sequence 2, Application US/09728137 Patent No. US20010029031A1
                                                                                                                     |:|| |:| : : | ||
838 SITHVNSLKLESECSAPG 855
```

```
Search completed: September 3, 2003, 11:53:44
Job time: 18.5 secs
                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                               Sequence 4, Application US/10274990
Publication No. US20030054491A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLOQ1018 DIV
CURRENT APPLICATION NUMBER: US/10/274,990
CURRENT FILING DATE: 2002-10-22
PRIOR REPLICATION NUMBER: 09/734,674
PRIOR FILING DATE: 2000-12-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09920804
Patent No. US20020064846A1
GENERAL INFORMATION:
APPLICANT: Selno, Susumu; JCR Pharmaceuticals Co., Ltd.
TITLE OF INVENTION: Sodium Ion-Driven Chloride/Bi-Carbonate Exchanger FILE REFERENCE: GP44
CURRENT APPLICATION NUMBER: US/09/920,804
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09920804
Patent No. US20020064846Al
GENERAL INFORMATION:
APPLICANT: Seino, Susumu; JCR Pharmaceuticals Co., Ltd.
TITLE OF INVENTION: Sodium Ion-Driven Chloride/Bi-Carbonate Exchanger
                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 47; DB 15; Length 1085; Pred. No. 36;
   Length 1085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
 Score 47; DB 9;
Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 47; DB 9;
Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                             |:|| |:| : : | ||
848 SITHVNSLKLESECSAPG 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:|| |:| : : | ||
851 SITHVNSLKLESECSAPG 868
                                                                          1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.08;
Query Match
Best Local Similarity 44.4%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.0%;
illarity 44.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 44.4'
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT;
; ORGANISM: Mus musculus
US-10-274-990-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Mus musculus US-09-920-804-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-920-804-2
                                                                                                                                                                                   US-10-274-990-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-920-804-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   848
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
                                                                                                                                                                  RESULT 13
                                                                          ò
                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
```

```
Gaps
                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                          Score 47; DB 9; Length 1088;
Pred. No. 36;
4; Mismatches 6; Indels
FILE REFERENCE: GP44
CURRENT APPLICATION NUMBER: US/09/920,804
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 4
LENGTH: 1088
                                                                                                                                                                                                                                                                                              |:|| |:| : | ||
851 SITHVNSLKLESECSAPG 868
                                                                                                                                                                                                                                                                        1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                            Query Match
Best Local Similarity 44.4%;
Matches 8; Conservative
                                                                                                                TYPE: PRT
ORGANISM: Homo sapience
US-09-920-804-4
```

; 0

THIS PAGE BLANK (USPTO)

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

September 3, 2003, 11:42:58; Search time 15.75 Seconds Run on:

(without alignments) 53.728 Million cell updates/sec

US-10-087-464-2 98 1 SVTHANALTVMGKASTPGAA 20 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

328717 segs, 42310858 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA: Database:

/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

4496, Ap 27116, A 4, Appli 2, Appli 18849, A 30365, A 5, Appli 9, Appli 11, Appli 11, Appli 11, Appli 11, Appli 11, Appli 11, Appli 11, Appli 11, Appli 11, Appli 12, Appli 12, Appli 13, Appli 14, Appli 15, Appli 16, Appli 17, Appli 17, Appli 18, Appli 19, Appli 10, Appli 11,	
esdaneuce sedane	
US-09-134-001C-4496 US-09-252-991A-27116 US-08-694-915-2 US-08-694-915-2 US-08-694-915-4 US-08-694-915-4 US-08-252-991A-30365 US-09-252-991A-30365 US-09-252-991A-19956 US-09-252-991A-19956 US-09-252-991A-19956 US-09-265-630-9 US-09-246-086-2 US-09-246-086-2 US-09-246-086-2 US-09-246-086-2 US-09-255-630-6	
44004445446444664	
886 340 416 416 421 421 151 151 153 333 333 363 363 363 452 452 452 452	
® M M M M M M M M M M M M M M M M M M M	
0	
22 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	

ALIGNMENTS

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                          Length 714;
                                                                                                                                                                                                                                                                                                                                                                                       e; Indels
                                                                                                                                                                                                                                                                                                                                                        48.0%; Score 47; DB 3;
44.4%; Pred. No. 7.4;
tive 4; Mismatches 6
                                  APPLICANT: Martin, Xavier
APPLICANT: Martin, Xavier
APPLICANT: Jupe, Steven C
APPLICANT: Rawlings, Christopher J
APPLICANT: Doe, Trudy R
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30409
CURRENT APPLICATION NUMBER: US/09/115,954B
           Sequence 4, Application US/09115954B Patent No. 6200776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/09115954B Patent No. 6200776
                                                                                                                                                                                                                                                                                                                                                                                                                                   |:|| |:| : : | || SITHVNSLKLESECSAPG 537
                                                                                                                                                                                                                                                                                                                                                                                                                 1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Khandoudi, Nassirah
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 44.4
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Boron, Walter F APPLICANT: Bril, Antoine M
                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
US-09-115-954-4
                                                                                                                                                                                                                                                                                                     PRT
                                                                                                                                                                                                                                                                                                                                                                                                                   δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                            a
```

```
TELEPHONE: 317-276-3334 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indianapolis
                                        Query Match
Best Local Similarity
Matches 8; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                    RESULT 5
US-09-734-674-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-734-674-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-926-327-2
  US-09-734-674-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
                                                                                                                      δλ
                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09734674

Patent No. 6498022
GENERAL INFORMATION:
APPLICANT: WEL, Ming-Hui et al
APPLICANT: WEL, Ming-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLO01018
FILE REFERENCE: CL001018
CURRENT APPLICATION NUMBER: US/09/734,674
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 1085
                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3; Length 1044;
12;
                                                                                                                                                                                                                Length 1032;
                                                                                                                                                                                                                                                         6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Indels
                                                                                                                                                                                                                  DB 3;
11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 47; DB 3
Pred. No. 12;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: BOTON, Walter F
APPLICANT: Bril, Antoine M
APPLICANT: Bril, Antoine M
APPLICANT: Martin, Navier
APPLICANT: Martin, Xavier
APPLICANT: Martin, Xavier
APPLICANT: Jupe, Steven C
APPLICANT: Bralings, Christopher J
APPLICANT: Boo, Trudy R
APPLICANT: Boo, Trudy R
APPLICANT: Doo, Trudy R
APPLICANT: DOO, Trudy R
FILE REFERENCE: GH-30409
CURRENT APPLICATION NUMBER: US/09/115,954B
CURRENT APPLICATION NUMBER: EP97401714.7
EARLIER APPLICATION NUMBER: EP97401714.7
EARLIER PILING DATE: 1997-07-16
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 2
SEQ ID NO 2
                                                                                                                                                                                                                Score 47; DB :
Pred. No. 11;
4; Mismatches
CURRENT FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: EP97401714.7
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09115954B Patent No. 6200776
                                                                                                                                                                                                                                                                                                                  |:|| |:| : : | ||
| 838 SITHVNSLKLESECSAPG 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:|| |:| : : | ||
850 SITHVNSLKLESECSAPG 867
                                                                                                                                                                                                                                                                                             1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SVTHANALTVMGKASTPG 18
                                  EARLIER FILING DATE: 1997-07-16
UNDBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.0%;
                                                                                                                                                                                                                Query Match
Best Local Similarity 44.4%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 48.0
Best Local Similarity 44.4
Matches 8; Conservative
                                                                                                                                  TYPE: PRT
CRGANISM: Homo sapiens
US-09-115-954-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
CRGANISM: Homo sapiens
US-09-115-954-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                  LENGTH: 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1044
                                                                                                                                                                                                                                                                                                                                                                                                                US-09-115-954-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-734-674-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
```

```
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL MIGHUN ET ALL
APPLICANT:
WELL MINENTION:
GENERAL MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION:
AND USES THEREOF
FILE REFERENCE: CL001018
CURRENT APPLICATION NUMBER: US/09/734,674
CURRENT FILING DATE:
SOFTWARE:
SOFTWARE:
FASTESQ for Windows Version 4.0
EDENGTH:
LENGTH:
LEN
                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .<u>.</u>
                                                                                                        ;
             Length 1085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1129;
                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08926327;
Patent No. 5821100
GENERAL INFORMATION:
APPLICANT: Baltz, Richard H.
APPLICANT: Solenberg, Patricia J.
TITLE OF INVENTION: Glycosyltransferase Gene gtfB From
TITLE OF INVENTION: Amycolatopsis Orientalis
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patentin Release #1.0, Version #1.30
                      4 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 47; DB 4;
Pred. No. 13;
DB
12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                        Mismatches
                  Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: P-10898
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/926,32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09734674 Patent No. 6498022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Lilly Corporate Center
                                                                                                                                                                                                                                                 |:|| |:| : | ||
848 SITHVNSLKLESECSAPG 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             892 SITHVNSLKLESECSAPG 909
                                                                                                                                                                                           1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
                  48.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
```

q

ò

```
APPLICANT: MCDANIEL, Robert
APPLICANT: TANG, Li
TITLE OF INVENTION: Combinatorial Polyketide Libraries Produced Using a
TITLE OF INVENTION: Modular PKS Gene Cluster as Scaffold
FILE REFERENCE: 300622002100
                                                                                APPLICANI: TANG, Li

TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 300622002120
; CURRENT APPLICATION NUMBER: US/09/320,878A
CURRENT FILING DATE: 1999-05-27
CURRENT FILING DATE: 1999-06-27
EARLIER APPLICATION NUMBER: CIP OF 09/141,908
EARLIER APPLICATION NUMBER: CIP OF 09/073,538
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1997-04-30
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1999-02-28
EARLIER FILING DATE: 1998-09-22
EARLIER FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 34

SOFTWARE: PATCHIN VOT: 2.0

SEQ ID NOS: 34

LENGTH: 4551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 4551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 4551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 42.9%; Score 42; DB 4; Length 455
Best Local Similarity 56.2%; Pred. No. 4.7e+02;
Matches 9; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 42.9%; Score 42; DB 3; Length 455
Best Local Similarity 56.2%; Pred. No. 4.7e+02;
Matches 9; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/141,908
CURRENT APPLICATION NUMBER: CIP OF 09/073,538
EARLIER FILING DATE: 1998-08-08
EARLIER FILING DATE: 1998-08-06
EARLIER FILING DATE: 1998-07-04
EARLIER FILING DATE: 1998-07-04
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER APPLICATION NUMBER: PROV. 60/076,919
EARLIER FILING DATE: 1998-03-05
EARLIER FILING DATE: 1998-03-05
EARLIER FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Streptomyces venezuelae
US-09-320-878-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT; ORGANISM: Streptomyces venezuelae
US-09-141-908-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09141908
Patent No. 6503741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4305 ASASTTAGTAGTPGTA 4320
                  APPLICANT: BETLACH, Melanie C. APPLICANT: BETLACH, Mary C. APPLICANT: MCDANIEL, ROBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 ANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: ASHLEY, GATY
APPLICANT: BETLACH, Melanie C. APPLICANT: BETLACH, MATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-141-908-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 407;
                                                                                                                                                      Ouery Match
Best Local Similarity 55.6%; Pred. No. 13;
Matches 10; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09119918
Patent No. 6025173
GENERAL INFORMATION:
APPLICANT: Baltz, Richard H.
APPLICANT: Solenberg, Patricia J.
TITLE OF INVENTION: Glycosyltransferase Gene gtfB From TITLE OF INVENTION: Amycolatopsis Orientalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/119,918.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 44; DB 3;
Pred. No. 13;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: P-10898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/926,327
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-320-878-1; Sequence 1, Application US/09320878A; Patent No. 6117659; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                             371 THARATAVAGTIRTDGAA 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       371 THARATAVAGTIRTDGAA 388
                                                                                                                                                                                                                                                                      3 THANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 THANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 55.6%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 407 amino acids amino acid
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-09-119-918-2
                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 46285
                                                                                                                    US-08-926-327-2
                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-119-918-2
```

; 0

Gaps

ö

; 0

Gaps

0

ò <u>8</u>

```
19103-2307
                                         APPLICANT: Sherman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-328-352-4650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
US-08-491-357-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                            Óγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                  | FACELIA NO. 20194323
| GENERAL INFORMATION:
| APPLICANT: ASHLEY, Gary
| APPLICANT: BETLACH, Melanie C.
| APPLICANT: BETLACH, Mary C.
| APPLICANT: BETLACH, Mary C.
| APPLICANT: TANG, Li
| TITLE OF INVENTION RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
| FILE OF INVENTION RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
| FILE OF INVENTION RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
| FILE REFERENCE: 300622001220
| CURRENT APPLICATION NUMBER: US/09/657,440
| CURRENT APPLICATION NUMBER: 1999-067
| PRIOR APPLICATION NUMBER: CIP OF 09/141,908
| PRIOR FILING DATE: 1999-06-27
| PRIOR FILING DATE: 1998-08-28
| NUMBER OF SEQ ID NOS: 34
| SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 4551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.9%; Score 42; DB 3; Length 4613; illarity 56.2%; Pred. No. 4.8e+02; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 42; DB 4; Lengtn 4.0...
Pred. No. 4.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Liu, Y.
APPLICANT: Zhao, Y.
APPLICANT: Shao, L.
TILLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 31, Application US/09105537A; Patent No. 6255202; GENERAL INFORMATION: APPLICANT: Sherman, D.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
US-09-105-537-6
; Sequence 6, Application US/09105537A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Streptomyces venezuelae
US-09-105-537-31
                                                                                                                                     Sequence 1, Application US/09657440 Patent No. 6509455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Streptomyces venezuelae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4305 ASASTTAGTAGTPGTA 4320
                    5 ANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 56.2%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 ANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 ANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 4613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 4551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-105-537-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-657-440-1
                                                                                                                    US-09-657-440-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
  ŏ
                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

```
Sequence 4650, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:
APPLICANT: GATUS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTE
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-0318
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4650
LENGTH: 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08491357
Patent No. 5716782
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Eaw, Susan
APPLICANT: Eaw, Susan
TITLE OF INVENTION: MEDIATOR PROTEIN THAT INDUCES CELLULAR MORPHOLOGICAL
TITLE OF INVENTION: ALTERATIONS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                             Length 11877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 819;
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Liu, Y.
APPLICANT: Liu, Y.
APPLICANT: Aleo, Y.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1988-06-26
NUMBER OF SEQ. ID NOS: 43
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ. ID NO 6
LENGTH: 11877
                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                        Query Match 42.9%; Score 42; DB 3; Best Local Similarity 56.2%; Pred. No. 1.4e+03; Matches 9; Conservative 1; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 40.8%; Score 40; DB 4; 1 Best Local Similarity 40.0%; Pred. No. 1.4e+02; Matches 8; Conservative 4; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SVTHANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                ORGANISM: Streptomyces venezuelae US-09-105-537-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Acinetobacter baumann11
US-09-328-352-4650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4703 ASASTTAGTAGTPGTA 4718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 ANALTVMGKASTPGAA 20
```

```
ò
                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Golemis, Erica A.
APPLICANT: Law, Susan
APPLICANT: Estolak, Johnne
TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING A SIGNAL
TITLE OF INVENTION: MEDIATOR PROTEIN THAT INDUCES CELLULAR.MORPHOLOGICAL
TITLE OF INVENTION: ALTERATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB 1; Length 872
Pred. No. 1.5e+02;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,633
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,357
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/491,357
                                                                                                                                                                                CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEPAX: (215) 563-404
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 872 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08968633 Patent No. 6100384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              473 STIVAHLLDLVGSASGPG 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 40.8%;
Best Local Similarity 50.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : ANTI-SENSE: NO
US-08-491-357-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-968-633-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

THIS PAGE BLANK (USPTO)

```
(without alignments)
156.918 Million cell updates/sec
                                                                                                                                                                                                   September 3, 2003, 11:46:23; Search time 17.5 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Ggn2_6/ptodata/I/Pubpaa/USG6_NEW_UBB.pep.*
'Ggn2_6/ptodata/I/Pubpaa/USG6_NEW_UBB.pep.*
'Ggn2_6/ptodata/I/Pubpaa/USG6_NEW_UBB.pep.*
'Ggn2_6/ptodata/I/Pubpaa/USG6_NEW_UBB.pep.*
'Ggn2_6/ptodata/I/Pubpaa/USG8_NEW_PUB.pep.*
'Ggn2_6/ptodata/I/Pubpaa/USG8_NEW_PUB.pep.*
'Ggn2_6/ptodata/I/Pubpaa/USG9_PUBCOMB.pep.*
'Ggn2_6/ptodata/I/Pubpaa/USG9B_PUBCOMB.pep.*
'Ggn2_6/ptodata/I/Pubpaa/USG9B_PUBCOMB.pep.*
'Ggn2_6/ptodata/I/Pubpaa/USG9B_PUBCOMB.pep.*
'Ggn2_6/ptodata/I/Pubpaa/USG9_PUBCOMB.pep.*
'Ggn2_6/ptodata/I/Pubpaa/USG9_PUBCOMB.pep.*
'Ggn2_6/ptodata/I/Pubpaa/USG10_PUBCOMB.pep.*
'Ggn2_6/ptodata/I/Pubpaa/USG10_PUBCOMB.pep.*
'Ggn2_6/ptodata/I/Pubpaa/USG10_PUBCOMB.pep.*
'Ggn2_6/ptodata/I/Pubpaa/USG10_PUBCOMB.pep.*
'Ggn2_6/ptodata/I/Pubpaa/USG10_PUBCOMB.pep.*
'Ggn2_6/ptodata/I/Pubpaa/USG0_NEW_PUB.pep.*
'Ggn2_6/ptodata/I/Pubpaa/USG0_NEW_PUB.pep.*
'Ggn2_6/ptodata/I/Pubpaa/USG0_NEW_PUB.pep.*
'Ggn2_6/ptodata/I/Pubpaa/USG0_PUBCOMB.pep.*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /ptodata/1/pubpaa/US07_PUBCOMB.pep:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         513375
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/1/pubpaa/US07
/cgn2_6/ptodata/1/pubpaa/PCT_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     513375 segs, 137303645 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0% .
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                              1 GKASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                   US-10-087-464-3
96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                       Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                       Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

escription	Sequence 3, Appli Sequence 22, Appl	Sequence 23,25, A Sequence 2, Appli	Sequence 8, Appli Sequence 7, Appli	Sequence 2, Appli	80 0	Sequence 4, Appli Sequence 39, Appl	Sequence 39, Appl Sequence 198, App
SUMMARIES	US-10-087-464-3 US-10-087-464-22 US-10-064-761-2020	US-10-066-320-2 US-10-087-464-6	US-10-087-464-8 US-09-963-896-7	US-10-087-464-2 US-09-808-880-3	US-09-764-891-3888 US-09-738-626-3894	US-10-054-562A-4 US-09-790-264-39	US-10-269-353-39 US-09-989-920-198
DB	15	15	15	113	11	14	15 10
% Query Match Length DB ID	20 42 65	911	911	3816	114	387	473 121
% Query Match	100.0	100.0	100.0	46.9	42.7	42.7	42.7
Score	96	9 6	96	44	41	414	41 40
Result No.	177) ፈ ቢ	9 /	ထော	10	12	14 15

Sequence 190, App Sequence 7573, Ap Sequence 13694, Ap Sequence 2064, Ap Sequence 11, Appli Sequence 19, Appli Sequence 19, Appli Sequence 19, Appli Sequence 14, Appli Sequence 17, Appli Sequence 17, Appli Sequence 3773, Ap Sequence 570, Appli Sequence 6609, Appli Sequence 6609, Appli Sequence 6600, Appli Sequence 670, Appli Sequence 670, Appli Sequence 770, Appli Sequence 150, Appli Sequence 160, Appli Sequence 162, Appli Sequence 77, Appli Sequence 162, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 501, Appli Sequence	Sequence 348, App Sequence 27, Appl
US-10-074-475-199 US-10-156-761-75 US-09-998-1027-1 US-09-998-027-1 US-09-998-027-1 US-09-998-027-1 US-09-998-027-1 US-09-988-127-1 US-09-881-279-14 US-09-881-579-14 US-09-881-579-14 US-09-881-579-14 US-09-881-579-14 US-09-881-579-14 US-09-881-579-14 US-09-881-579-14 US-09-738-626-51 US-09-867-550-150 US-09-867-550-150 US-09-867-550-150 US-09-867-550-150 US-09-867-550-150 US-09-867-550-150 US-09-867-550-150 US-09-738-626-51 US-09-867-550-150 US-09-867-550-150 US-09-738-626-51 US-09-867-550-150 US-09-738-626-51	15 US-10-153-668-348 10 US-09-971-798-27
122 190 190 190 190 190 190 190 190 190 190	239 343
444444444444444444444 HIHHHHHHOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO	39.6 39.6
60000000000000000000000000000000000000	38
. 111112222222222222222222222222222222	44 45

GEMERAL INFORMATION: APPLICANT: Chishti, Athar APPLICANT: Chishti, Athar APPLICANT: Liu, David APPLICANT: Liu, Liu, Nuerong TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses There FILE REFERENCE: \$1237/7019 CURRENT APPLICATION NUMBER: US/10/087,464 CURRENT FILING DATE: 2002-03-01 PRIOR APPLICATION NUMBER: US 06/272,930 PRIOR FILING DATE: 2001-03-02 NUMBER OF SEQ ID NOS: 59 SEQ ID NO 3 LENGTH: 20 Sequence 3, Application US/10087464 Publication No. US20030059436A1

ALIGNMENTS

US-10-087-464-3

Gaps ; 0 Length 20; Indels Score 96; DB 15; Pred. No. 1.4e-08; ch 100.0%; Score 96; DB Similarity 100.0%; Pred. No. 1.4 20; Conservative 0; Mismatches Query Match Best Local Similarity Matches

ORGANISM: Homo sapiens

US-10-087-464-3

ö

1 GKASTPGAAQIQEVKEQRI 20 qq Qγ

RESULT 2
US-10-087-464-22
Sequence 22, Application US/10087464
Sequence No. US20030059436A1
GENERAL INFORMATION:

```
INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
INFORMATION: SWISSPROT HIT: P02730, EVALUE 3.00e-21
INFORMATION: EST_HUMAN HIT: BF526005.1, EVALUE 3.00e-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 96; DB 9; Length 86;
Pred. No. 7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gow, Andrew J.
APPLICANT: Singel, David J.
TITLE OF INVENTION: Method for Determining Physiological
TITLE OF INVENTION: Method for Determining Physiological
TITLE OF INVENTION: Effects of Hemoglobin
FILE REPERENCE: 1818.1030-003
CURRENT APPLICATION NUMBER: US/10/066,320
CURRENT FILING DATE: 2002-01-31
PRIOR FILING DATE: 2002-01-31
PRIOR FILING DATE: 1999-08-02
PRIOR FILING DATE: 1999-08-02
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR PELING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 33328
LENGTH: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 96; DB 15; ilarity 100.0%; Pred. No. 1e-06; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IN PLACENTA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Scu-
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10066320 Publication No. US20030022267A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GKASTPGAAAQIQEVKEQRI 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/10087464 Publication No. US20030059436A1 GENERAL INFORMATION: APPLICANT: Chishti, Athar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GKASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GKASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Stamler, Jonathan S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 100...
The 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , ORGANISM: Homo sapiens
US-10-066-320-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
CTHER INFORMATION: M.
OTHER INFORMATION: E.
OTHER INFORMATION: J.
OTHER 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 911
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-087-464-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
APPLICANT: Liu, David
APPLICANT: Goel, Vikas
APPLICANT: Li, Xuerong
TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
FILE REFERENCE: 81237/7019
CURRENT APPLICATION NUMBER: US/10/087,464
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 06/272,930
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn version 3.0
SEQ ID NO 22
LENGTH: 42
TYPE: LENGTH: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; DB 15;
. 3.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 00/20/, 430
PRIOR PLLING DATE: 2000-05-26
PRIOR PLLING DATE: 2000-08-03
PRIOR PLLING DATE: 2000-08-03
PRIOR PLLING DATE: 2000-10-04
PRIOR PLLING DATE: 2000-09-27
PRIOR PLLING DATE: 2000-09-27
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PLLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PLLING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2001-01-30
APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 39328, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GKASTPGAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 100.0%;
L Similarity 100.0%;
20; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR
PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
```

Gaps

ö

Gaps

o;

```
APPLICANT: Oh, Steven
APPLICANT: Liu, David
APPLICANT: Liu, David
APPLICANT: Liu, Xuerong
TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses There
FILE REPERENCE: 51237/7019
CURRENT APPLICATION NUMBER: US/10/087,464
CURRENT FILING DATE: 2002-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IND PC COMPATIBLE
COMPUTER: IND PC COMPATIBLE
COMPUTER: DE-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
PPLLICATION NUMBER: US/09/963,896
FILING DATE: 26-Sep-2001
CLASSIFFCATION: GUNROWN>
PRIOR APPLICATION: GUNROWN>
APPLICATION DATA:
APPLICATION NUMBER: 09/397,558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 50; DB 10;
Pred. No. 28;
5; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 15;
                                                                                                                                                                                                                                                                                                         FILING DATE: <Unknown>
ATTORREY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0527 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.9%; Score 45; DB 100.0%; Pred. No. 1.6 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.1%; Score 50; 60.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; SEQUENCE DESCRIPTION: SEQ ID NO: 7 US-09-963-896-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 06/272,930
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 59
SOFTWARRE PATENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1317 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/10087464 Publication No. US20030059436A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | ||:||:||:||:
448 GAASSPGSAARLQEL 462
                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GKASTPGAAAQIQEV 15
                     STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 100.00
Free 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Chishti, Athar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GKASTPGAA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-087-464-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 2
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ol, Steven
APPLICANT: Liu, David
APPLICANT: Liu, David
APPLICANT: Liu, David
APPLICANT: Liu, Mass
APPLICANT: 2002-03-01
CURRENT APPLICANT: NUMBER: US, 06/272,930
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.0
                                    APPLICANT: Goel, Vikas
APPLICANT: Li, Xuerong
TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lal, Preeti
Guegler, Karl J.
Corley, Neil C.
TITLE OF INVENTION: PROSTATE GROWTH-ASSOCIATED MEMBRANE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                     Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                   Score 96; DB 15;
Pred. No. 1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 96; DB 15;
Pred. No. 1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: INCYTE PHARMACEUTICALS, INC
                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                             FILE REFERENCE: $1237/7019
CURRENT APPLICATION NUMBER: US/10/087,464
CURRENT FILING DATE: 2002-03-01
PRIOR PLLING DATE: 2001-03-01
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GKASTPGAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/10087464 Publication No. US20030059436A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GKASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09963896
Patent No. US20020102585Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Some Best Local Similarity 100.0%; P. Matches 20; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Chishti, Athar
                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-10-087-464-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                       Liu, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                            SEQ ID NO 6
LENGTH: 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-087-464-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-087-464-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-06-69-896-7
                                                                                                                                                                                                                                                                                    TYPE: PRT
APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
```

g

```
Sequence 4, Application US/10054562A;
Sequence 4, Application US/10054562A;
Publication No. US20020165375A1
GENERAL INFORMATION:
APPLICANT: Chandrashear, Ramaswamy
APPLICANT: Chandrashear, THEREOF
TITLE OF INVENTION: PARASITIC HELMINTH CUTICLIN PROTEINS, NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: THEREOF
FILE REFERENCE: HW-8-2
CURRENT APPLICATION NUMBER: US/10/054,562A
CURRENT FILING DATE: 2002-06-10
PRIOR PAPLICATION NUMBER: 09/812,642
PRIOR PAPLICATION NUMBER: 09/812,642
PRIOR PAPLICATION NUMBER: 09/323,427
PRIOR PAPLICATION NUMBER: 09/323,427
SPRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Version 3.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.7%; Score 41; DB 10; Length 345; 50.0%; Pred. No. 1.7e+02; tive 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41; DB 14; Length 387; Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                         APPLICANT: ANIZOGOLII, HINCSHI,
APPLICANT: ANIZOGOLII, HINCSHI,
APPLICANT: HAYASHI, MIKIRO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: SENGH, AKHHIRO
APPLICANT: SENGH, AKHHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKI
TITLE REFERENCE: 249-125
CURRENT FILING DATE: 2000-12-18
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
SPRIOR PRILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 3894
                                                                                                                                                                     Sequence 3894, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Corynebacterium glutamicum US-09-738-626-3894
                                                                                                                                                                                                                                               APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SELKO
APPLICANT: HAYASHI, MIKTRO
APPLICANT: OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 ASTPGAAAQIQEVKEQ 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 ASTDGTASRLLELKEK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Dirofilaria immitis
US-10-054-562A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.0v
  2 KASTPGAAAQIQ 13
                                               16 QASTPGAALAVO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                              US-09-738-626-3894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-054-562A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ωp
                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (88)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-891-3888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                   Sequence 3, Application US/0980880

Publication No. US2003002728741

GERERAL INFORMATION:

APPLICANT: Betlach, Mary C.

APPLICANT: Betlach, Sanjay Krishnakant

APPLICANT: Betlach, Expert

APPLICANT: Tang, Li

TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE

FILE REPERENCE: 30062-20029.00

CURRENT APPLICATION NUMBER: US/09/808,880

CURRENT FILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: US/09/428,517

PRIOR PLILING DATE: 1999-02-16

PRIOR PPLICATION NUMBER: 60/120,254

PRIOR FILING DATE: 1999-02-16

PRIOR PLILING DATE: 1999-10-29

NUMBER OF SEQ ID NOS: 12

SEQ ID NO 3

LENGTH: 3816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: Recombinant; OTHER INFORMATION: Oleandolide PKS
US-09-808-880-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3888. Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.8%; Score 44; DB 11; Length 3816; 60.0%; Pred. No. 8.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.7%; Score 41; DB 11; Length 114;
66.7%; Pred. No. 48; 2; Indels
tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | ||| | :||| :|
1412 SIPGALASLQEVLDQ 1426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 STPGAAAQIQEVKEQ 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
12 GKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity
Matches 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-764-891-3888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
```

ŏ

ö

Gaps

Page

us-10-087-464-3.rapb

```
RESULT 15
US-09-989-920-198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                              FATERIC NO. USLOUZOUZED A.

APPLICANT: GOOGGEALL ANGINE A.

APPLICANT: HOLTZMAN DOUGLAS A.

APPLICANT: GOOGGEALL ANGINE D.J.

APPLICANT: GOOGGEALL ANGINE D.J.

APPLICANT: MCCARTLY, Sean A.

TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING

TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING

TITLE OF INVENTION: USES

FILE REFERENCE: 07334-322001

CURRENT APPLICATION NUMBER: US 09/065,661

PRIOR APPLICATION NUMBER: US 09/065,661

PRIOR APPLICATION NUMBER: US 09/065,333

PRIOR FILING DATE: 1999-04-23

PRIOR FILING DATE: 1999-04-23

PRIOR FILING DATE: 1999-06-22

PRIOR FILING DATE: 1999-07-29

PRIOR FILING DATE: 1999-07-29

PRIOR FILING DATE: 1999-07-29

PRIOR APPLICATION NUMBER: US 09/124,538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SERIEMATE INCLUENCE AND ADDRIVE HOLIZORNI GOOGGATI, AND APPLICANT: HOLIZORNI GOOGGATI, AND APPLICANT: GOOGGATI, AND AND APPLICANT: GOOGGATI, AND AND APPLICANT: GOOGGATI, AND ADDRICANT: MCCATCHY, SCAN A.

TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: USES
TITLE OF INVENTION: USES
TITLE OF INVENTION: USES
CURRENT APPLICATION NUMBER: US 10/70269, 353
CURRENT APPLICATION NUMBER: US 09/790, 264
PRIOR APPLICATION NUMBER: US 09/790, 264
PRIOR FILING DATE: 2001-02-21
PRIOR FILING DATE: 1998-04-23
PRIOR FILING DATE: 1998-04-23
PRIOR FILING DATE: 1999-04-23
PRIOR FILING DATE: 1999-04-23
PRIOR FILING DATE: 1999-04-23
PRIOR FILING DATE: US 09/065, 363
  ö
     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.4e+02;
5; Indels
  Indels
     4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9;
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 42.7%; Score 41;
Best Local Similarity 47.1%; Pred. No. 3
Matches 8; Conservative 4; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 39, Application US/10269353 Publication No. US20030104447A1 GENERAL INFORMATION:
                                                                                                                                                                                                                         Sequence 39, Application US/09790264 Patent No. US20020028508A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Drosophila melanogaster
US-09-790-264-39
                                                                                 1 |: | ||||: : :|::
283 GAAAKPAAAAQLRLLKKR 300
6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | ||:||:| ::|
292 GAASSPGSAHQSNAIEE 308
                                                 1 GKASTPGAAAQIQEVKEQ 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GKASTPGAAAQIQEVKE 17
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-269-353-39
.;
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
Matches
                                                                                              g
                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

```
APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Chen, Sei-Yu
APPLICANT: Chen, Sei-Yu
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and P
FILE REPERENCE: DEX-0291
CURRENT APPLICATION NUMBER: US/09/989,920
CURRENT FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: 60/252,500
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 284
SOFTWARE: PatentIn version 3.1
SEQ ID NO 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                 ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                          Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10; Length 121;
                                                                                                                                                                                                                                                                                                                  42.7%; Score 41; DB 15; Length 47
47.1%; Pred. No. 2.4e+02;
Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
               PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: US 09/102,705
PRIOR FILING DATE: 1998-06-22
PRIOR FILING DATE: 1998-07-29
PRIOR FILING DATE: 1999-07-29
PRIOR PRIOR PILING DATE: 1999-07-29
PRIOR FILING DATE: 1998-07-29
NUMBER: OF SEQ ID NOS: 68
SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: September 3, 2003, 11:53:44
Job time: 17.5 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.7%; Score 40; 40.0%; Pred. No.
08/337,930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 198, Application US/09989920 Patent No. US20020172957A1
                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-269-353-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                    | ||:||:| ::|
292 GAASSPGSAHQSNAIEE 308
                                                                                                                                                                                                                                                                                                                                                                                                                         1 GKASTPGAAAQIQEVKE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GKASTPGAAAQIQEV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 GSSSSPASASOVAEI 43
                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 47.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Macina, Roberto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapien
US-09-989-920-198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 6; Conserv
```

THIS PAGE BLANK (USPTO)

us-10-087-464-3.rai

```
Sequence 2083; A Sequence 23893, A Sequence 22320, A Sequence 32336, A Sequence 2, Appli Sequence 2, Appli Sequence 31292, A Sequence 31292, A Sequence 29728, A Sequence 11, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2338, A Sequence 27338, A Sequence 27338, A Sequence 27338, A Sequence 27338, A Sequence 28169, A Sequence 20548, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/09083521
Patent No. 6048970
GENERAL INFORMATION
APPLICANT: Lal, Preeti
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Nell C.
TITLE OF INVENTION: PROSTATE GROWTH-ASSOCIATED MEMBRANE PROTEINS
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 1317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 194304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/083,521
FILING DATE: Herewith
CLASSIFICATION:
                      US-09-252-991A-23693
US-09-252-991A-22320
US-09-252-991A-32336
US-09-252-991A-18394
US-09-479-309-2
US-09-627-393-2
US-09-252-991A-31292
US-09-252-991A-31292
                                                                                                                        US-09-252-991A-28148
US-09-252-991A-29728
US-08-978-289-12
US-09-601-478-1
US-09-601-478-4
US-09-252-991A-28169
US-09-252-991A-28169
US-09-252-991A-28169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.1%; Score 50; DB 60.0%; Pred. No. 8.9; ive 5; Mismatches
                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0527 US
TELECOMUNICATION INFORMATION:
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS,
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GKASTPGAAAQIQEV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 60.0%
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        639
704
937
89
239
239
282
330
400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LIBRARY: GenBank
; CLONE: 2459993
US-09-083-521-7
US-09-083-521-7
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Appli
Sequence 32531, A
Sequence 22504, A
Sequence 3, Appli
Sequence 24458, A
Sequence 30223, A
Sequence 4, Appli
Sequence 4, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11, Appl
18921, A
3757, Ap
1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Appl
Appl
Appl
Appl
Appl
Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Appl
Sequence 19, Appl
Sequence 30395, A
Sequence 21037, A
Sequence 31986, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                 (without alignments) 53.728 Million cell updates/sec
                                                                                    3, 2003, 11:42:58 ; Search time 15.75 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Sequence 11 Sequence 11 Sequence 11 Sequence 11 Sequence 12 Sequence 18 Sequence 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence
                                                                                                                                                                                                                                                                                                                                                                      Issued_Patents_AA:*
.: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
          GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-252-991A-32531
US-09-252-991A-32504
US-09-252-991A-31069
US-09-252-991A-31069
US-09-252-991A-3023
US-09-323-427-4
US-09-323-427-4
US-09-323-427-4
US-09-69-253-11
US-09-69-253-11
US-09-69-253-11
US-09-469-253-11
US-09-107-532A-3757
US-09-319-980-4
US-09-412-11
US-09-612-342-11
US-09-612-342-11
US-09-612-342-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -09-252-991A-30395
-09-252-991A-21037
-09-252-991A-31986
                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                              328717 segs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                            OM protein - protein search, using sw model
                                                                                                                                                               1 GKASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                               length: 0
length: 2000000000
                                                                                                                                US-10-087-464-3
96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyright
                                                                                     September
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                   Perfect score:
                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41
                                                                                                                                                                                                                                                                                Minimum DB
Maximum DB
                                                                                                                                                                                                                              Searched:
                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                         Database
                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10
111
112
113
114
117
118
118
119
119
119
125
125
126
127
127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Result
                                                                                                                                        Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
```

g

```
TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE FILE REFERENCE: 30062-20029.00
CURRENT APPLICATION NUMBER: US/09/428,517
CURRENT FILING DATE: 1999-10-28
EARLIER APPLICATION NUMBER: 60/120,254
EARLIER FILING DATE: 1999-02-16
EARLIER FILING DATE: 1998-10-29
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.8%; Score 42;
ilarity 50.0%; Pred. No.
Conservative 3; Mismatcl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 31069, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24458, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ||| | :||| :|
1412 SIPGALASLQEVLDQ 1426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||| ||: :|| :
206 TPGAVAQLHGEEEQAV 221
                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 TPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 STPGAAQIQEVKEQ 18
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 60.0v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
...... 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION: APPLICANT: Marc J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
US-09-252-991A-31069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
US-09-252-991A-24458
                                                                                                                                                                                                                                                                        LENGTH: 3816
                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22504, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22564
LENGTH: 490
                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERCIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32531
LENGTH: 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45; DB 4; Length 577;
Pred. No. 23;
5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.4%; Score 44.5; Ilarity 50.0%; Pred. No. 23; Conservative 5; Mismatches
                                                                                                         Sequence 32531, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09428517
Patent No. 6251636
GENERAL INFORMATION:
APPLICANT: Betlach, Mary C.
APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: McDaniel, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:| || || ||:|:|:|
94 GRADQPG-AAEVQQVRRQ 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :||| || |::| ::||
191 QASTHGADAELQPLREQ 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GKASTPGAAQIQEVKEQ 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KASTPGAAAQIQEVKEQ 18
448 GAASSPGSAARLQEL 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 52.9%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-252-991A-22504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Pseudo
US-09-252-991A-22504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-428-517-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
```

ò

g

```
GENERAL INFORMATION:
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERGIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ACID AND ACID AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AEROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: Recombinant; OTHER INFORMATION: Oleandolide PKS
US-09-428-517-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.8%; Score 44; DB 3; 1 60.0%; Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ed. No. 32;
Mismatches
```

m

;;

```
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Morales, Tony H.
TITLE OF INVENTION: Parasitic Helminth Cuticlin Proteins, Nucleic Acid
TITLE OF INVENTION: Molecules, and Uses Thereof
FILE REFERENCE: HW-8
         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
      ;0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41; DB 4; Length 387; Pred. No. 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP STREET: P.O. Box 747 CITY: Falls Church STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,286
         4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: NAKAMURA, SELJI
APPLICANT: SAKURAI, TAKASHI
APPLICANT: NEZU, JUNI-ICHI
TITLE OF INVENTION: GENE ENCODING ADSEVERIN
WUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
         6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/812,642
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 09/323,427
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11, Application US/08669286 Patent No. 6130060
                                                                                                                                                                                                     Sequence 4, Application US/09812642 Patent No. 6368600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: MURRHY Jr., Gerald M.
REGISTRATION UNDRER: 28,977
REFERENCE/DOCKET NUMBER: 230-
TELECOMMUNICATION INFORMATION:
TELEFAM: (703) 205-8000
TELEFAM: (703) 205-8050
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                            283 GAAAKPAAAQLRLLKKR 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           283 GAAAKPAAAQLRLLKKR 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GKASTPGAAAQIQEVKEQ 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
                                                1 GKASTPGAAQIQEVKEQ 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Dirofilaria immitis
US-09-812-642-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 44.4%;
Matches 8; Conservative
      8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 22040-0747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-669-286-11
                                                                                                                                                                                US-09-812-642-4
      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196_136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER: OS 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Morales, Tony H.

TITLE OF INVENTION: Parasitic Helminth Cuticlin Proteins, Nucleic Acid
TITLE OF INVENTION: Molecules, and Uses Thereof
TITLE OF INVENTION: Molecules, and Uses Thereof
CURRENT APPLICATION NUMBER: US/09/323,427
CURRENT FILING DATE: 1999-06-01
EARLIER APPLICATION NUMBER: 60/087,435
BARLIER FILING DATE: 1998-06-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                Score 42; DB 4; Length 343; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 42; DB 4; Length 362;
Pred. No. 42;
5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB 3; Length 387;
Pred. No. 66;
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                 2; Mismatches
PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 24458
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 30223, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:|: || | :: :| ||
98 GRAADPGTGATVRLAEEGRI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GKASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09323427
Patent No. 6248329
                                                                                                                                                                                                                                                                                                                                       218 RAETPGAAALAAAVPQR 235
                                                                                                                                    ) ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                             2 KASTPGAAAQIQEVKEQR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.78;
                                                                                                                                                                                                  Query Match
Best Local Similarity 50.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 43.8%;
Best Local Similarity 40.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Dirofilaria immitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-252-991A-30223
                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-252-991A-30223
                                                                                          LENGTH: 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-323-427-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-323-427-4
                                                                                                                                                                                                                                                                                                                                       op,
                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

; 0

```
INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.7%; Score 41; DB 3; Length 827;
43.8%; Pred. No. 1.6e+02;
tive 5; Mismatches 4; Indels
                                                                                                                    Length 827;
                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                              Sequence 11, Application US/09469253

Sequence 11, Application US/09469253

GENERAL INFORMATION:
APPLICANT: NAKAWURA, SEIJI
APPLICANT: SAKURAL, TAKASHI
APPLICANT: NEZU, JUNI-ICHI
TITLE OF INVENTION: GENE ENCODING ADSEVERIN
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITT: Falls Church
CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CUBRENT APPLICATION DATA: APPLICATION NUMBER: US/09/469,253 FILING DATE:
                                                                                                                  42.7%; Score 41; DB 3; 343.8%; Pred. No. 1.6e+02; tive 5; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/669,286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: MURPHY Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 230-110P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 11, Application US/09642146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION: (703) 205-8000
TELEFAX: (703) 205-8000
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 827 amit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                          359 GKTHTVGSVAKVEQVK 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GKASTPGAAAQIQEVK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GKASTPGAAAQIQEVK 16
amino acids
                                                                                                      Ouery Match
Best Local Similarity 43.89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                              ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-669-286-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
              TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 7; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-642-146-11
                                                                                                                                                                                                                                                                                             US-09-469-253-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-469-253-11
LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
                                                                                                                                                                                                                                                                              RESULT 11
                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
```

```
Sequence 18921, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICAMTION:
APPLICAMTION
AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
APPLICANT: NAKAMURA, SEIJI
APPLICANT: NAKAMURA, SEIJI
APPLICANT: SAKURAI, TAKASHI
APPLICANT: SAKURAI, TAKASHI
APPLICANT: SAKURAI, TAKASHI
APPLICANT: NEZU, JUNI-ICHI
TITLE OF INVENTION: GENE ENCODING ADSEVERIN
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/642,146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41; DB 3;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230-110P
                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/669,286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 230-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        || | |: |::::||
359 GKTHTVGSVAKVEQVK 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 42.7%;
Best Local Similarity 43.8%;
Matches 7; Conservative !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GKASTPGAAAQIQEVK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            827 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-09-642-146-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-252-991A-18921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
```

```
Search completed: September 3, 2003, 11:52:29 Job time: 17.75 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | | | | : |: | | ::||
21 GNASSSGSLQQISTLREQ 38
                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                        Sequence 3757, Application US/09107532A
Patent No. 6583375
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLETC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: BUTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; LOCATION: (252),(292)
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-252-991A-18921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ÷
                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                     DB 4; Length 460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 137;
                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB 4;
Pred. No. 30;
5; Mismatches. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 40.5; DE
; Pred. No. 97;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAME/KEY: misc_feature incorporation: 137 incorporation: SEQUENCE DESCRIPTION: SEQ ID NO: 3757: US-09-107-532a-3757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-9277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
COUNTRY: USA
ZIP: 02364
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.7%; Scor.
36.8%; Pred
5; '
                                                                                                                                                                       193 GRRDAPGASGEVOGEEVEOR 212
                                                                                                                                       1 GKASTPGAAQIQ-EVKEQR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 137 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 3757:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KASTPGAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 KMSSPGVVPLLDSLKEEKI 25
                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 7310
                                                                   Query Match 42.2%;
Best Local Similarity 45.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 7; Conserva
                                                                                                                                                                                                                                          US-09-107-532A-3757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE
                                                                                                                                                                                                                        RESULT 14
                                                                                                                                        ŏ
                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
```

```
APPLICANT: Trixeira De Mattos, Maarten J.
APPLICANT: Blom, Jolanda
TITLE OF INVENTION: METHODS FOR MODULATING METABOLIC PATHWAYS OF
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
FILE REFERENCE: 24615-20123.00
CURRENT PILING DATE: 1999-06-114
CURRENT APPLICATION NUMBER: PCT/NL97/00688
EARLIER APPLICATION NUMBER: PCT/NL97/00688
EARLIER FILING DATE: 1999-12-12
BARLIER FILING DATE: 1996-12-12
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: HAP3
US-09-319-989-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
41.7%; Score 40; DB 3; Length 144;
Best Local Similarity 44.4%; Pred. No. 31;
Matches 8; Conservative 4; Mismatches 6; Indels
Sequence 4, Application US/09319989 Patent No. 6190914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GKASTPGAAAQIQEVKEQ 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
```

THIS PAGE BLANK (USPTO)

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

September 3, 2003, 11:46:23 ; Search time 17.5 Seconds Run on:

(without alignments)
156.918 Million cell updates/sec

US-10-087-464-4

112 1 DRILLLFKPPKYHPDVPVK 20 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

513375 seqs, 137303645 residues Searched:

513375 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published_Applications_AA:*

/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

/cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:# /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:# /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:# /ptodata/1/pubpaa/US10B_PUBCOMB.pep: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:* /cgn2_6/ptodata/1/pubpaa/USO70_LEW_UB.pep:* /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:* /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:* /cgn2_6/ptodata/1/pubpaa/USO8A_PUBCOMB.pep: /cgn2_6/ptodata/1/pubpaa/USO9A_PUBCOMB.pep://cgn2_6/ptodata/1/pubpaa/USO9A_PUBCOMB.pep: cdn2

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*/cgn2_6/ptodata/1/pubpaa/US10_NRW_PUB.pep:*/cgn2_6/ptodata/1/pubpaa/US60_NRW_PUB.pep:*/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

SUMMARIES

	Description	Sequence 4, Appli	Sequence 23, Appl	Sequence 2, Appli	Sequence 6, Appli	Sequence 8, Appli	Sequence 34894, A	Sequence 1, Appli	Sequence 44, Appl	Sequence 2, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 373, App	Sequence 2, Appli	Sequence 176, App
4	110	US-10-087-464-4	US-10-087-464-23	US-10-066-320-2	US-10-087-464-6	US-10-087-464-8	US-09-864-761-34894	US-09-747-804-1	US-09-908-805B-44	US-09-920-804-2	US-09-920-804-4	US-09-734-674-2	US-10-274-990-2	US-10-205-823-373	US-09-732-020-2	US-09-811-284-176
.6	a ;	15	15	15	15	15	σ	6	10	6	6	σ	15	15	σ	6
6 4 4	Match Length DB	20	51	911	911	911	26	336	542	1088	1088	1129	1129	1035	578	186
& Query	Match	100.0	100.0	100.0	100.0	100.0	55.4	46.4	44.6	43.8	43.8	43.8	43.8	42.9	41.1	40.2
Š	score	112	112	112	112	112	62	52	20	49	49	49	49	48	46	45
Result		٦	7	m	4	S	٥	7	æ	6	10	11	12	13	14	15

20, App 20, App 20, App 20, App 33, App 118, App 112, App 112, App 112, App 112, App 112, App 113, App 114, App 115, App 116, App 117, App 118, App	Seguence 8, Appli
0.0-177-809 99-965-529 99-965-529 99-965-529 99-965-528 99-975-806 99-975-143 99-975-143 99-975-143 99-975-143 99-975-143 99-975-143 99-975-143 99-975-143 99-975-143 99-975-143 99-975-143	9 US-09-728-137-8
0444018 111122222222222222222222222222222222	1032
44400000000000000000000000000000000000	38.4
N N N 4 4 N N N N N N N N N N N N N N N	43
110 110 110 110 110 110 110 110 110 110	45

ALIGNMENTS

```
APPLICANT: Oh, Steven
APPLICANT: Liu, David
APPLICANT: Liu, David
APPLICANT: Liu, David
APPLICANT: Liu, David
APPLICANT: Liu, Nuerong
TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses There
FILE REFERENCE: $1237/7019
CURRENT APPLICATION NUMBER: US/10/087,464
CURRENT APPLICATION NUMBER: US 06/272,930
PRIOR PILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 112; DB 15;
Pred. No. 9e-10;
; Mismatches 0;
Sequence 4, Application US/10087464
Publication No. US20030059436A1
GENERAL INFORMATION:
APPLICANT: Chishti, Athar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; S
Best Local Similarity 100.0%; P
Matches 20; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-087-464-4
```

RESULT 2
US-10-087-464-23
Sequence 23, Application US/10087464
Publication No. US20030059436Al
GENERAL INFORMATION: 1 DRILLLFKPPKYHPDVPYVK 20 1 DRILLEKPPKYHPDVPYVK 20 q δ

ö

Gaps

.; 0

Indels

```
APPLICANT: CHISCANCE,
APPLICANT: Ob, Steven
APPLICANT: Liu, Steven
APPLICANT: Liu, Steven
APPLICANT: Goel, Vikas
APPLICANT: Li, Xuerong
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INCORDATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION TO SENE EXPRESSION ANALYSIS BY MICROARRAY
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                               Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                            ; DB 15;
4.8e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; DB 15;
4.8e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 112; DE
Pred. No. 4.8e
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            Score 112;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: $1237/7019
CURRENT APPLICATION NUMBER: US/10/087,464
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 06/272,930
PRIOR FILING DATE: 2001-03-02
                                US/10/087,464
                         CURRENT APPLICATION NUMBER: US/10/087,46
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 06/272,930
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 34894, Application US/09864761 Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           807 DRILLEKPPKYHPDVPYVK 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DRILLLFKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/10087464
Publication No. US20030059436Al
GENERAL INFORMATION:
APPLICANT: Chishti, Athar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DRILLLEKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
      FILE REFERENCE: S1237/7019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn versic
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-087-464-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-10-087-464-8
                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-864-761-34894
                                                                                                                                                                                                                                                   LENGTH: 911
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                 APPLICANT: Goel, Vikas
APPLICANT: Goel, Vikas
APPLICANT: Li, Xuerong
TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
CURRENT APPLICATION NUMBER: US/10/087,464
CURRENT FILING DATE: 2002-03-01
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 59
SEQ ID NOS: 59
SEQ ID NO 23
LENGTH: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Oh, Steven
APPLICANT: Liu, David
APPLICANT: Goel, Vikas
APPLICANT: Li, Xuerong
TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION.

APPLICANT: Stamler, Jonathan S.

APPLICANT: Stamler, Jonathan S.

APPLICANT: Gow, Andrew J.

TITLE OF INVENTION: Method for Determining Physiological TITLE OF INVENTION: Effects of Hemoglobin FILE REFERENCE: 1818.1030-003

CURRENT APPLICATION NUMBER: US/10/066,320

CURRENT APPLICATION NUMBER: PCT/US00/21101

PRIOR PRING DATE: 2000-08-02

PRIOR PELING DATE: 2000-08-02

PRIOR FILING DATE: 1999-08-02

PRIOR FILING DATE: 1999-08-02

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 100.0%; Score 112; DB 15; Similarity 100.0%; Pred. No. 2.4e-09; 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 112; DB 15;
Pred. No. 4.8e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               807 DRILLEKPPKYHPDVPYVK 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/10087464
Publication No. US20030059436A1
GENERAL INFORMATION:
APPLICANT: Chishii, Athar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DRILLFKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/10066320 Publication No. US20030022267A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DRILLERRPRYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 100.(
Matches 20; Conservative
Chishti, Athar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-066-320-2
                                                             Liu, David
                                Oh, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-087-464-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 2
LENGTH: 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-087-464-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
```

ò g ö

RESULT 4

ò g ő

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Seino, Susumu; JCR Pharmaceuticals Co., Ltd.
TITLE OF INVENTION: Sodium Ion-Driven Chloride/Bi-Carbonate Exchanger
                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.6%; Score 50; DB 10; Length 542; 47.4%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                               Length 336;
                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: METCALF, DONALD
APPLICANT: NICOLA, NICOS A
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC AGENTS
    TITLE OF INVENTION: EXTRACELLULAR ADHESIVE PROTEINS
                                                                                                                                                                                                                                                                                                                               DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/908,805B CURRENT FILING DATE: 2001-07-19
                 FILE REFERENCE: PF-0576 US
CURRENT APPLICATION NUMBER: US/09/747,804
CURRENT FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                 Score 52;
Pred. No.
                                              PRIOR APPLICATION NUMBER: 2000-12-22
PRIOR APPLICATION NUMBER: 09/131,648
PRIOR FILING DATE: 1998-08-10
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PERL PROGRAM
TEMPORAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 08/962,560
PRIOR FILING DATE: 1997-10-31
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 44, Application US/09908805B Patent No. US20020147307A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09920804 Patent No. US20020064846A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (94'); OTHER INFORMATION: Xaa is unsure US-09-908-805B-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DRILLEKPPKYHPDVPYV 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WILLSON, Tracey A
RICHARDSON, Rachael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STARR, Robyn
NICHOLSON, Sandra E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HILTON, Douglas J
APPLICANT: ALEXANDER, Warren S
APPLICANT: VINEY, Elizabeth M
                                                                                                                                                                                                                                                                                                                               46.4%;
ilarity 57.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       37 ILQPPVFHPVVPYV 50
                                                                                                                                                                                                                                                                                                                                                                                                                6 LFKPPKYHPDVPYV 19
                                                                                                                                                                                                                                                         ; OTHER INFORMATION: 2635136
US-09-747-804-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 47.4
Matches 9; Conservative
                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 8; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 109762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-908-805B-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
US-09-920-804-2
                                                                                                                                                                                       LENGTH: 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE868202.1, EVALUE 3.00e-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IN LUNG, SIGNAL = 1.1
IN ADDLT LIVER, SIGNAL = 1.9
IN BT474, SIGNAL = 2.3
IN FETAL LIVER, SIGNAL = 4.6
IN HELA, SIGNAL = 4.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIT: 018917, EVALUE 1.00e-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLACENTA, SIGNAL = 2.2
HBL100, SIGNAL = 1.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEART, SIGNAL = 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 9;
0.047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                      PRIOR FILING DATE: 2000-09-20
PRIOR PELICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-09-27
PRIOR PLICATION NUMBER: PCT/USO1/00667
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/USO1/00669
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2000-09-21
PRIOR PRILING DATE: 2000-09-21
PRIOR PRILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 62;
Pred. No.
APPLICATION NUMBER: US 09/632,366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: MAP TO AC009955.1 OTHER INFORMATION: EXPRESSED IN BONE
                                      APPLICATION NUMBER: GB 24263.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09747804
Patent No. US20010010913A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 RILLEKPPKYHPDVPYV 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yue, Henry
Corley, Neil C.
Guegler, Karl J.
Patterson, Chandra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXPRESSED :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST_HUMAN
SWISSPROT
                                                             FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 55.6'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-864-761-34894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 34894
LENGTH: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-747-804-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER
OTHER
OTHER
OTHER
OTHER
OTHER
OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
```

δ g

```
APPLICANT: WEI, Ming-Hui et al TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS, TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS, TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: CLOO1018 DIV CURRENT APPLICATION NUMBER: US/10/274,990 CURRENT FILING DATE: 2002-10-22 PRIOR APPLICATION NUMBER: 09/774,674 PRIOR FILING DATE: 2000-12-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.9%; Score 48; DB 15; Length 1035;
                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                               Sequence 2, Application US/10274990 Publication No. US20030054491A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DRILLLFKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.8%;
ilarity 45.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Human
US-10-274-990-2
                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1129
                                            JS-10-274-990-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09734674
Patent NO. US20020081648A1
GENERAL INFORMATION:
TITLE OF UNENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/734,674
CURRENT APPLICATION NUMBER: US/09/734,674
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09920804

Patent No. US20020064846A1

GENERAL INFORMATION:
APPLICART: Sealno, Susumu; JCR Pharmaceuticals Co., Ltd.
TITLE OF INVENTION: Sodium Ion-Driven Chloride/Bi-Carbonate Exchanger:
FILE REFERENCE: GP44

CURRENT APPLICATION NUMBER: US/09/920,804

CURRENT FILING DATE: 2001-08-03

NUMBER OF SEQ ID NOS: 8

LENGTH: 1088
                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                         Score 49; DB 9; Length 1088;
Pred. No. 79;
4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 49; DB 9; Length 1088;
Pred. No. 79;
4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 49; DB 9; Length 1129;
Pred. No. 83;
4; Mismatches 7; Indels
FILE REFERENCE: GP44
CURRENT APPLICATION NUMBER: US/09/920,804
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 2
LENGTH: 1088
                                                                                                                                                                                                                                                                                                              |||| | : | |: || |::
DRIKLFWMPAKHQPDFIYLR 946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||| | : | |: || |::
DRIKLFWMPAKHQPDFIYLR 987
                                                                                                                                                                                                                                                                                         1 DRILLLFKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DRILLLFKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DRILLEKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.8%;
45.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.8%;
                                                                                                                                                                                                      Query Match 43.8%;
Best Local Similarity 45.0%;
Matches 9; Conservative '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 45.03
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 45.0
Matches 9: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CRGANISM: Homo sapience
US-09-920-804-4
                                                                                                                        ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-920-804-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                             US-09-920-804-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-734-674-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

Indels

Length 1129;

Score 49; DB 15; Pred. No. 83; 4; Mismatches 7

```
IDENTIFICATION, ASSESSMENT, PREVENTION, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Zhao, xumel APPLICANT: Zhao, xumel APPLICANT: Daderson, Dustin TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND TITLE OF INVENTION: THERAPY OF PROSTATE CANCER FILE DEFERENCE: MRI-044
CURRENT APPLICATION NUMBER: US/10/205,823
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR PAPLICATION NUMBER: 60/314,356
PRIOR PAPLICATION NUMBER: 60/314,456
PRIOR PELING DATE: 2001-09-25
PRIOR PELING DATE: 2001-09-25
PRIOR PELING DATE: 2001-102-12
PRIOR PELING DATE: 2001-12-12
PRIOR FILING DATE: 2001-12-13
                                                                                                                                                                                                                                                                                       Sequence 373, Application US/10205823
Publication No. US20030108963A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
Hoersch, Sebastian
Kamatkar, Shubhangi
Wonsey, Angela M.
Glatt, Karen
Zhao, Xumei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gannavarapu, Manjula
Gorbatcheva, Bella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endege, Wilson O.
```

```
US-09-811-284-176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                         ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 176, Application US/09811284

Fatent No. US20020058306A1

GENERAL INFORMATION:

APPLICANT: Vogeli, Gabiel

TITLE OF INVENTION: No. US20020058306A1e1 G Protein-Coupled Receptors

FILE REPERENCE: 001670S1

CURRENT APPLICATION NUMBER: US/09/811,284

CURRENT FILING DATE: 2001-03-16

PRIOR PLILING DATE: 2000-03-16

PRIOR APPLICATION NUMBER: 60/189,907

PRIOR FILING DATE: 2000-03-16

PRIOR PLILIATION NUMBER: 60/189,918

PRIOR PLILIATION NUMBER: 60/189,960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                           Gaps
                         ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 46; DB 9; Length 5/6.
Pred. No. 1.1e+02;
  Pred. No. 1.1e+02;
4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                             N: Human Oxalyl-CoA Decarboxylase
PF119D3
                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/732,020
CURRENT FILING DATE: 2000-12-08
PRIOR FILING DATE: 1999-06-03
PRIOR FILING DATE: 1999-06-03
PRIOR FILING DATE: 1997-06-03
PRIOR PELICATION NUMBER: 08/458,120
PRIOR PELICATION NUMBER: 08/458,120
PRIOR APPLICATION NUMBER: 08/458,120
PRIOR PELING DATE: 1995-06-02
PRIOR PELING DATE: 1995-06-02
PRIOR PELING DATE: 1995-06-02
PRIOR FILING DATE: 1995-06-03
PRIOR FILING DATE: 1905-06-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R FILING DATE: 2000-03-16
R APPLICATION NUMBER: 60/189,917
R FILING DATE: 2000-03-16
R APPLICATION NUMBER: 60/192,945
R FILING DATE: 2000-03-29
R APPLICATION NUMBER: 60/192,916
                                                                                                                                                                                                                     Sequence 2, Application US/09732020
Patent No. US20010003743A1
GENERAL INFORMATION:
APPLICANT: Henrik, Olsen
APPLICANT: Timothy, Coleman
APPLICANT: Mark, Adams
TITLE OF INVENTION: Human Oxalyl-CC
FILE REFERENCE: PF119D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/192,923
FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/192,933
                                                                                            ||:|| || |:|| |:|
880 DRLKLLLMPLKHQPDFIYLR 899
                                                                   1 DRILLLFKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn version 3.0
Best Local Similarity 45.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||:| ||| :::
292 PPRYQPDVKFIQ 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 РРКҮНРБУРУУК 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: HOMO SAPIENS US-09-732-020-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-811-284-176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Fa
SEQ ID NO 2
LENGTH: 578
                                                                                                                                                                             RESULT 14
US-09-732-020-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR
                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                     δý
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
```

THIS PAGE BLANK (USPTO)

```
US-08-446-777-4
406
 40.2
45
28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                    September 3, 2003, 11:42:58; Search time 15.75 Seconds (without alignments) 53.728 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                         328717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                    328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STIMMARTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                  US-10-087-464-4
112
1 DRILLLFKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4. . . . .
```

Title: Perfect score: Sequence:

Run on:

Scoring table:

Searched:

Database :

RIES	Description	5-647B-43 Sequence 43, App.	3 Sequence 43,	3 Sequence 43,	Sequence 9, A	Sequence 9,	Sequence 9,	15	Sequence 1,	4 Sequence 24,	Sequence 44,	Sequence 2, 1	Sequence 8,	Sequence 8,	Sequence 2,	80	Sequence 2,	Sequence 2,	Sequence 2,	Sequence 2,	14 Sequence 14,	Sequence 14,	4 Sequence 1	Sequence 2, P	Sequence 2,	Sequence 2,	Sequence 2,	-18 Section 18
SUMMARIES	ID	US-08-405-647B-	US-08-985-499-4	PCT-US96-03180-4	US-08-405-647B-9	US-08-985-499-9	PCT-US96-03180-9	US-08-269	US-09-131-648-1	US-09-012-504A-	US-09-30	US-09-734-674-2	ns-08-66	US-09-143-438-8	US-09-136	US-08-476-509B	US-08-464	US-08-464-604A-2	US-08-87	ns-08-903	US-08-405-647B-	US-08-985-499-1	PCT-US96-03180-1	US-08-458-120-	-026-867-970-	US-09-326-217-2	US-09-732-020-	TS-08-102
	DB		٣	'n	٣	m	Ŋ	-	٣	4	4	4	~	m	٣	m		~	~	7	m	m	Ŋ	7	7	e	4	C
	Length	58	58	58	14	14	14	11	336	119	542	1129	376	376	1079	169	147	147	147	147	7	7	7	578	578	578	578	340
æ	Query	100.0	100.0	100.0	70.5	70.5	70.5	61.6	46.4	•	44.6	43.8	42.9	42.9	42.9	42.4	41.5	41.5	41.5	41.5	41.1	41.1	41.1	41.1	41.1	41.1	41.1	40.2
	Score	112	112	112	79	79		69	52	20	20		48	48	48	47.5	46.5	46.5	46.5	46.5	46	46	46	46	46	46	46	4.5
	Result No.	1	7	e	4	2	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27

1 DRILLLFKPPKYHPDVPYVK 20

QΥ

					0;
4, Appli 6, Appli 8, Appli 18, Appli 18, Appli 7, Appli 16, Appli 6, Appli 6, Appli 11, Appli 11, Appli 11, Appli 4, Appli 4, Appli 2, Appli 11, Appli 11, Appli 11, Appli 11, Appli 11, Appli 11, Appli 12, Appli 13, Appli 14, Appli 15, Appli 16, Appli 17, Appli 17, Appli 18, Appli 18, Appli 11, A					Gaps
sedneuce sed		ells			8;
8 9 8 9 8 9 8 9 8 9 8 9 8 8 8 8 8 8 8 8		Reducing 1 Blood Ce			Length 58 Indels
		COL REC	.30		0
7-64 -7-8 -7-8 -7-8 -7-11 -7-11 -7-11 -7-4 -7-4 -7-4 -7-4 -	70	thods fo ective R Crew LLP h Floor	lon #1	snc	DB 3 1.1e-1
4466-777 -4466-777 -4466-777 -4066-604 -4066-604 -4066-604 -4066-904 -4066-904 -4067-904 -	ALIGNMENTS 47B	Marie nd Me f Def and and	, Version	.068700	Score 112; Pred. No. 1 : Mismatche
US-08-446-777-4 US-08-446-777-6 US-08-446-777-8 US-08-446-604A-8 US-09-795-926-18 US-09-795-926-12	ALIC	. Jear ions ness wnser nter,	s-Dos #1.0	77 N: S:	Score Pred 0; Mis
111104044444440400000	70840	⊞ C α α . · ·	lsk atibl 00s/v lease : 5/08/ 995	900 6	
400 767 767 162 162 184 188 321 332 333 333 1032 1032	=	Sherman, Irwin W. Crandall, Ian E. Sholet, Stephen B Thevenin, Bernard WENTION: Composit VENTION: Adhesive EQUENCES: 50 TWO EMDESS: TOWNSENS: TOWNSENG and TO TWO Embarcadero Ce in Francisco	ZIP: 94111-3834 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN PREJEASE #1.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/405,6. FILING DATE: 17-WAR-1995 CLASSIFICATION: 514 ATTORNEY/AGENT INFORMATION: NAME: Weber, Kenneth A.	RECISTRATION NUMBER: 31,677 REFERENCE/DOCKET NUMBER: TELECOMMULICATION INFORMATION: TELEFAX: (415) 576-0200 TELEFAX: (415) 576-0300 FORMATION FOR SEQ ID NO: 43: SEQUENCE CHARACTERISTICS: LENGTH: 58 amino acids TYPE: amino acids STRANDEDNESS: TOPOLOGY: linear MOLECULE TYPE: peptide	100.0%; 100.0%; vative
4446 W E W E W E W E W E W E W E W E W E W	licat 162 TION:	APPLICANT: Sherman, Ir APPLICANT: Crandall, I APPLICANT: Thevenin, B TITLE OF INVENTION: Co TITLE OF INVENTION: Co NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS: 5 CORRESPONDENCE ADDRESS: 5 CAPPENDENCE ADDRESS: 5 CITY: San Francisco STREET: Two Embarcad CITY: San Francisco STATE: California	ZIF: 94111-3834 MEDUTER READABLE FORM MEDIUM TYPE: Flopp) COMPUTER: IBM PC CC COMPUTER: IBM PC CC SOFFWARE: PATENTIN SYSTEM: I SOFTWARE: PATENTIN APPLICATION UNMER: CILLING DATE: 17-MAR CLASSIFICATION: 51/ COMMENTARY NAME: Weber, Kennet	RECISTRATION NUMBER: REFERENCE/DOCKET NUMBER: TELEPHONE: (415) 576-0 TELEFAX: (415) 576-0 FORMATION FOR SEQ ID NO SEQUENCE CHARACTERISTIC LENGTH: 58 amino acil TYPE: amino acid STRANDEDNESS: TOPOLOGY: linear TOPOLOGY: linear TOPOLOGY: linear TOPOLOGY: linear	Similarity 0; Conser
	APF APF 51242 FORMA	S S S S S S S S S S S S S S S S S S S	94111 READA TYPE ER: ING SA ING SA RE: APPLICATION ATION DATE FICATION	AATION WCE/DO NICATON WCE/DO NICATON K: (4 N FOR CHARA : 58 : 58 : maino SINESS 3-43	Simi]
4 4 4 4 4 4 5 6 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	4 4 CH	APPLICANT: S APPLICANT: S APPLICANT: T TITLE OF INVE NUMBER OF SEQ CORRESPONDENC ADDRESSEE: STREET: Tw CITY: San STATE: Cal COUNTRY: Cal	ZIP: 94111-383 COMPUTER READBALE MEDIUM TYPE: F COMPUTER: IBM OPERATING SYSTE SOFTWARE: PET STEE TURN APPLICATION NUM FILING DATE: 17 CLASSIPICATION: ATTORNEY/AGENT IN NAME: WEDELT K	RECISTRATION REFERENCE/DO TELECOMMUNICAT TELEPHONE: TELEPHONE: TELEPATION FOR SEQUENCE CHARA LENGTH: 58 TYPE: amino STRANDENNESS TOPOLOGY: 1 MOLECULE TYPE: 405-647B-43	/ Match Local S nes 20
2228 3322 3322 3323 34444444 352 362 362 362 362 362 362 362 362 362 36	RESULT 1 US-08-405-647B-43 Sequence 43, Applica' Patent No. 6124262 GENERAL INFORMATION	APPLIC APPLIC APPLIC TITLE TITLE TITLE CORRES ADDR STRE STAT COUN	CON W CON	REFERENCE/DO REFERENCE/DO TELEPHONE: TELEPANIE: TELEPANIE: TELEPANIE: TELEPANIE: SEQUENCE CHARA SEQUENCE CHARA TYPE: amin STRANDEDNES: TOPOLOGY: MOLECULE TYPE: MOLECULE TYPE:	Query Match Best Local Matches 2
	#D * * * *				
			-	•	

```
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 576-020
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity.
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US96-03180-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-405-647B-9
                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: The Regents of the University
APPLICANT: of California
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REDUCING
TITLE OF INVENTION: ADHESIVENESS OF DEFECTIVE RED BLOOD CELLS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                     APPLICANT: Shohet, Stephen B.
APPLICANT: Sherman, Irwin
APPLICANT: Sherman, Irwin
APPLICANT: Sherman, Irwin
APPLICANT: Von Andrian, Ulrich
TITLE OF INVENTION: Methods for Enhancing Thrombolysis in a
TITLE OF INVENTION: Mammal
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
RILING DATE: US/08/985,499
FILING DATE: US-DEC-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 112; DB 3; 100.0%; Pred. No. 1.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Robbins, Berliner & Carson
STREET: 201 North Figueroa Street, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 05-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hyman, Laurence J.
REGISTRATION NUMBER: 35,551
REFERENCE/DOCKET NUMBER: 02307E-084500US
TELECHOME: (415) 576-030
TELEPHONE: (415) 576-0300
TELEPHONE: (415) 576-0300
TELERAX: (415) 576-0300
INFORMATION FOR SED ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 anino acids
TYPE: amino acid
STREE: amino acid
STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 43, Application PC/TUS9603180 GENERAL INFORMATION:
                                                                                                       Sequence 43, Application US/08985499
Patent No. 6191103
GENBELI INFORMATION:
APPLICANT: Shohet, Stephen B.
                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 DRILLERPPKYHPDVPYVK 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DRILLLEKPPKYHPDVPYVK 20
DRILLLFKPPKYHPDVPYVK 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-985-499-43
                                                                                                                                                                                                                                                                                                                                                                       San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT-US96-03180-43
                                                                                    US-08-985-499-43
                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sherman, Irwin W.
APPLICANT: Crandall, Ian E.
APPLICANT: Crandall, Ian E.
APPLICANT: Theorem. Sholet, Stephen B.
APPLICANT: Theorem. Bernard Jean-Marie
TITLE OF INVENTION: Compositions and Methods for Reducing
TITLE OF INVENTION: Adhesiveness of Defective Red Blood Cells
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                      Length 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                      Score 112; DB 5;
Pred. No. 1.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Weber, Kenneth A. REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 02307E-068700US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                     APPLICATION NUMBER: US/08/405,647B
FILING DATE: 17-MAR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/03180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/08405647B Patent No. 6124262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DRILLLFKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 DRILLEKPPKYHPDVPYVK 27
                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
100.0%;
```

```
COPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/03180
FILING DATE:
CLASSIFICATION NUMBER: PCT/US96/03180
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: BETLINGT, ROBERT
REGISTRATION NUMBER: 25.5-370
TELEPHONE: (213) 977-1003
TELEPHONE: (213) 977-1003
TELEPHONE: (213) 977-1003
TELEPHONE: CLASSIFICS:
SEQUENCE CHARACTERISTICS:
LENTH: 1.14 manio acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/269,441A
FILING DATE: 30-JUN-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5; Le
. 3.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rearden, Ann
TITLE OF INVENTION: A NOVEL AUTOANTIGEN, PINCH
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREPT: 4225 Executive Square, Suite 1400
CITY: Los Angeles
STATE: California
    Robbins, Berliner & Carson 201 North Figueroa Street, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 92037
COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-269-441A-15; Sequence 15, Application US/08269441A; Pattent to 552529; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 30-JUN 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HALLE Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFRENCE/COCKT NUMBER: 0725;
TELECOMMUNICATION INFORMATION:
TELEPAX: (619) 678-509
TELEPAX: (619) 678-509
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                             COUNTRY: USA
ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KPPKYHPDVPYVK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 КРРКҮНРБУРУУК 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
                        STREET: 201 North
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US96-03180-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application PC/TUS9603180
GENERAL INFORMATION:
APPLICANT: The Regents of the University
APPLICANT: of California
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REDUCING
TITLE OF INVENTION: ADHESIVENESS OF DEFECTIVE RED BLOOD CELLS
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                      Sequence 9, Application US/08985499
Patent No. 6191103
GENEAL INFORMATION:
APPLICANT: Sherman, Irwin
APPLICANT: Sherman, Irwin
APPLICANT: VON Andrian, Ullich
TITLE OF INVENTION: Methods for Enhancing Thrombolysis in a
TITLE OF INVENTION: Ammmal
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                         Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 14;
                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,499
FILING DATE: 05-DEC-1997
CLASSIFICATION: 514
                                      Score 79; DB 3; L
Pred. No. 3.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 79; DB 3; L
Pred. No. 3.2e-06;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Hyman, Laurence J.
REGISTRATION NUMBER: 35.551
REFERENCE/DOCKET NUMBER: 02307E-084500US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 9:
                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                      70.5%; Scc.
100.0%; Pre
0; '
                                                                                                                                         1 KPPKYHPDVPYVK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 KPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
                                      Query Match 70.5
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-985-499-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: CZ
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US96-03180-9
US-08-405-647B-9
                                                                                                                                                                                                                     RESULT 5
US-08-985-499-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                    å
                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            õ
```

Gaps ő

Length 14; Indels

Gaps

; 0

Length 119;

```
GENERAL INFORMATION:
APPLICANT: WEI, Ming-Hui et al
APPLICANT: WEI, Ming-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REPERENCE: CLO01018
CURRENT APPLICATION NUMBER: US/09/734,674
CURRENT FILING DATE: 2000-12-13
                                          NAME/KEY: misc_feature
LOCATION: (103)..(103)
OTHER INFORMATION: The 'Xaa' at location 103 stands for Asp, Gly, Ala, or Val.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: STARR NODYN
APPLICANT: NICHOLSON, Sandra E
APPLICANT: NICHOLSON, Sandra E
APPLICANT: NICHOLSON, Sandra E
APPLICANT: NICHOLSON, Sandra E
APPLICANT: NICHOLA, NICOS A
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC AGENTS
FILE REFERENCE: 10976Z
CURRENT APPLICATION NUMBER: US/09/302,769
PRIOR APPLICATION NUMBER: 08/962,560
PRIOR FILING DATE: 1997-10-31
                                                                                                                                                                                                                                     DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                 44.6%; Score 50; DB 53.3%; Pred. No. 1.2; tive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 50;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 44, Application US/09302769 Patent No. 6323317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09734674
Patent No. 6498022
                                                                                                    FEATURE:

NAME/KEY: misc_feature

COATION: (1)..(662)

COTHER INFORMATION: n=a, c, g, or

US-09-012-504A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Xaa is unsure US-09-302-769-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DRILLLFKPPKYHPDVPYV 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RICHARDSON, Rachael T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HILTON, Douglas J
APPLICANT: AFRANDER, Warren S
APPLICANT: VINEY, Elizabeth M
APPLICANT: WILLSON, Tracey A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 47.4%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                   2 RILLLFKPPKYHPDV 16
                                                                                                                                                                                                                                                                                                                                          |:| |:|| :||:|
71 RMLFKFEPPLFHPNV 85
                                                                                                                                                                                                                                 Query Match
Best Local Similarity 53.3
Matches 8; Conservative
      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin Ve
SEQ ID NO 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: UNSURE LOCATION: (94)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-302-769-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-734-674-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3; Length 336;
                                                                                                                                                                                        Length 11;
                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GS-09-012-504A-24

Sequence 24, Application US/09012504A

FRACE No. 6464974

GENERAL INFORMATION:
APPLICANT: Berlin, V.
APPLICANT: Chiu, I.
APPLICANT: Damagnez, V.
FILE REFERENCE: APBI-P05-036

CURRENT APPLICATION NUMBER: US/09/012,504A

CURRENT FILING DATE: 1998-01-23

PRIOR FILING DATE: 1994-12-20

FRICK APPLICATION NUMBER: 08/360,144

PRIOR FILING DATE: 1994-12-20

FRICK APPLICATION NUMBER: 08/250,795

FRICK APPLICATION NUMBER: 08/250,795

NUMBER OF SOU IN NOS: 35

SOFTWARE PATENTING DATE: 1994-05-27

NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Butterson, Chandra
TITLE OF INVENTION: EXTRACELLULAR ADHESIVE PROTEINS
FILE REFERENCE: PF-0576 US
                                                                                                                                                                                        Score 69; DB 1; L
Pred. No. 8.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ed. No. 1.9;
Mismatches
                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/131,648
CURRENT FILING DATE: 1998-08-10
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PERL Program
SEQ ID NO 1
LENGTH: 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 52;
Pred. No.
                                                                                                                                                                         61.6%; Sco.
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09131648 Patent No. 6168920
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.4%;
ilarity 57.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 LFKPPKYHPDVPYV 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE: -
; OTHER INFORMATION: 2635136
US-09-131-648-1
                                                                                                                                                                                        Query Match 61.6
Best Local Similarity 100.
Matches 11; Conservative
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                               1 FKPPKYHPDVP 11
                                                                                                                                                                                                                                                                          7 FKPPKYHPDVP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                    ), NAME/KEY: Peptide
; LOCATION: 1..11
US-08-269-441A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                US-09-131-648-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 24
LENGTH: 119
                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               염
```

ö

Gaps

; 0

Length 542; Indels

```
FILING DATE:
                                                                                                                                                                                                 D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-143-438-8
 US-09-143-438-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                              ö
                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/08666367B
Patent No. 5854042
GENERAL INFORMATION:
APPLICANT: Shuichi TSUJI et al.
TITLE OF INVENTION:
PRODUCING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                              ;
0
                                                                                                                             Length 1129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                              7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: D.C.
COUNTRY: U.S.A.
IP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/666,367B
FILING DATE: AUGUST 19, 1996
CLASSIFICATION: 435
                                                                                                                                 Score 49; DB 4;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Wenderoth, Lind & Ponack STREET: Wenderoth, Lind & Ponack CITY: Washington STATE: D.C. COUNTRY: U.S. A. ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48;
Pred. No.
                                                                                                                                                                                                                    968 DRIKLFWMPAKHQPDFIYLR 987
                                                                                                                                                                                              1 DRILLERPPKYHPDVPYVK 20
                                                                                                                             Query Match
43.8%; So
Best Local Similarity 45.0%; Pr
Matches 9; Conservative 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||:|: | || |:|
223 ILILWDPSVYHADIP 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 ILLLFKPPKYHPDVP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 11
                                                                              ; ORGANISM: Human
US-09-734-674-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM:
US-08-666-367B-8
                                                                                                                                                                                                                                                                              RESULT 12
US-08-666-367B-8
                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                              ð
```

RESULT 13

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                         GENERAL INFORMATION:
APPLICANT: Shuichi TSUJI et al.
TITLE OF INVENTION: NOVEL SUGAR-CHAIN SYNTHETASE AND PROCESS FOR TITLE OF INVENTION: PRODUCING THE SAME
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3;
                                                                                                                                                                          ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P. STREET: 2033 K Street, N.W., #800
                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: BRILL, ANTOINE
APPLICANT: BRILL, ANTOINE
APPLICANT: RHANDOUDI, NASSIRAH
APPLICANT: BARTIN: XAVIER
TITLE OF INVERTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30010
CURRENT APPLICATION NUMBER: US/09/136,652A
CURRENT FILING DATE: 1998-08-19
EARLIER PAPLICATION NUMBER: EP 974019473.3
EARLIER FILING DATE: 1997-08-19
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 48; DB
Pred. No. 9.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          TOWBER: US/09/143,438 August 28, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-09-136-652-2
Sequence 2, Application US/09136652A
; Partent No. 6096517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/666,367
FILING DATE: August 19, 1996
ATTORNEY/AGENT INFORMATION:
NAME: WALTEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08/666,367
Sequence 8, Application US/09143438 Patent No. 6218161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223 ILILWDPSVYHADIP 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 ILLLEKPPKYHPDVP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 202-721-8250
                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                      CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: mouse
```

```
APPLICANT: SUDOL, MARIUS
APPLICANT: PEER, BORK
APPLICANT: PEER, BORK
APPLICANT: HENRY, CHEN
TITLE OF INVENTION: A SH2 DOMAIN ASSOCIATED PROTEIN, A
TITLE OF INVENTION: SIGNALLING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF ADDRESSE: 50
CORRESPONDENCE ADDRESS: ABORESSE: Alauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                               ö
                                                                                                                               Gaps
                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
42.4%; Score 47.5; DB 3; Length 169;
Best Local Similarity 47.6%; Pred. No. 4.4;
Matches 10; Conservative 1; Mismatches 5; Indels
                                                                                DB 3; Length 1079; 30;
                                                                                                                           7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IDM PC compatible
CORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,509B
FILING DATE: 01-DEC-1994
CLASSIFICATION:
ATTORNEY/AGENT INVESTMENTON:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 600-1-101 CIP
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 201 343-1684
                                                                                  Score 48; DB 3; Pred. No. 30; 4; Mismatches
                                                                                                                                                                                                                                                                                           US-08-476-509B-28; Sequence 28, Application US/08476509B; Patent No. 6034212
                                                                                                                                                                                              924 DRLKLLLMPLKHQPDFIYLR 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 RILLLFKPPKY----HPDVP 17
                                                                                                                                                                  1 DRILLEFKPPKYHPDVPYVK 20
                                                                                  Query Match
Best Local Similarity 45.0%;
Matches 9; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 13351
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 169 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-476-509B-28
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-136-652-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
ZIP: 07601
                                                                                                                                                                    ò
                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

Search completed: September 3, 2003, 11:52:29 Job time: 15.75 secs

```
5.1.6
Compugen Ltd.
 GenCore version
Copyright (c) 1993 - 2003
```

OM protein - protein search, using sw model

September 3, 2003, 11:41:03; Search time 17.25 Seconds Run on:

(without alignments)
111.500 Million cell updates/sec

US-10-087-464-1 104 1 GMPWLSATTVRSVTHANALT 20 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 Total number of hits satisfying chosen parameters:

283308 seqs, 96168682 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir1:* pir2:* pir3:* pir4:* PIR_76:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

-	Description	d 3 ani	band 3 anion trans	m	anion transporter	band 3 anion trans	band 3 anion trans	band 3 anion trans	band 3 protein, no	band 3-related pro	band 3-related pro	band 3-related pro	anion exchange pro	anion exchanger 3,	band 3-related pro	erythrocyte anion	anion exchanger 3	band 3 anion trans	hypothetical prote	probable lipoic ac	sodium bicarbonate	sodium bicarbonate	sodium bicarbonate	Na+ bicarbonate co	sodium bicarbonate	hypothetical prote	hypothetical prote	cobalamin biosynth	diacylglycerol kin	probable sodium bi
SUMMARIES	ID	A33810	взно	A25314	150159	A30816	S59861	S24318	A25104	A34911	A31789	A56764	S21086	A42497	B34911	A33638	I38496	S31828	T28858	T44895	T31336	T13962	T14110	PC7034	T14031	C72506	B72722	F69000	æ	T37460
	DB	7	Н	7	7	~	7	~	7	~	~	7	~	7	~	~	7	7	7	~	~	7	7	~	7	~	7	7	~	7
	Query Match Length	848	911	929	844	922	912	918	865	1234	1237	1237	1240	1030	1227	1227	1232	357	826	314	1035	1035	1035	1079	1079	156	111	302	727	1119
æ	Query		100.0	100.0	96.2	96.2	91.3	91.3	89.4		89.4	89.4	89.4	85.6	85.6	85.6	85.6	80.8			45.2	45.2	٠	•	45.2			43.3	43.3	43.3
	Score	104	104	104	100	100	95	95	93	93	93	93	93	88	88	68	83	84	53	48	47	47	47	47	47	46	45	45	45	45
	Result No.	1	7	e	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote probable cytochrom	hypothetical prote hypothetical prote	NADH2 dehydrogenas	probable liboic ac	hypothetical prote	PHO85-like protein	u-plasminogen acti	cytochrome c-type	hypothetical prote	cytochrome c-type	iron binding prote	hypothetical prote	glycine betaine/L-
T22491 H70526	T27828 T27829	T11840	C70787	T22841	T42379	UKHU	E57987	D86101	н91260	T45065	D83563	MMECPW
0.0	0 0	2 (4 (4	7	7	Н	Н	7	7	7	7	7
1175	1508 1519	115	311	387	415	431	552	552	552	332	350	354
43.3	42.3	41.3	41.3	41.3	41.3	41.3	40.9	40.9	40.9	40.4	40.4	40.4
45 44	4 4 4 4	43	4.4	43	43	43	42.5	42.5	42.5	42	42	42
30 31	3 3 3 3	34	36	37	38	39	40	41	42	43	. 44	45

ALIGNMENTS

```
Cydrosesion: A33810
R:Kudrycki, K.E.; Shull, G.E.
J. Balol. Chem. 264, 8185-819.
J. Biol. Chem. 264, 8185-819.
J. File: Primary structure of the rat kidney band 3 anion exchange protein deduced fr A; Reference number: A33810; MUID:89255254; PMID:272777
A; Status: preliminary
A; Status: preliminary
A; Status: Preliminary
A; Residues: 1-848 < KUD>
A; Cross-references: GB:J04793; NID:g203092; PIDN:AAA40800.1; PID:g203093
C; Superfamily: band 3 anion transport protein
C; Keywords: alternative splicing; transmembrane protein
                                                       C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 104; DB 2; Length 848; 100.0%; Pred. No. 8.3e-09; Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GMPWLSATTVRSVTHANALT 20
                                - rat
A33810
band 3 anion transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.C
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δλ
```

ö

RESULT 2

657 GMPWLSATTVRSVTHANALT 676

g

Danid 3 anion transport protein, erythrocyte - human
N;Alternate names: carrier family 4, anion exchanger, member 1; erythroid anion excha
C;Species: Homo sapiens (man)
C;Date: 03-Mug-1984 #sequence_revision 03-Oct-1995 #text_change 22-Jun-1999
C;Accession: A36218; S03074; I39408; I39409; A92237; A26507; A92430; A90323; A28079;
R;Lux, S.E.; John, K.M.; Kopito, R.N.; Lodik, H.F.
Proc. Natl. Acad. Sci. U.S.A. 86, 9089-9003s, H.F.
Proc. Natl. Acad. Sci. U.S.A. 86, 9089-9003s, 1989
A;Title: Cloning and characterization of band 3, the human erythrocyte anion-exchange A;Reference number: A36218; MUID:90083213; PMID:2594752
A;Status: preliminary

A; Molecule type: mRNÅ A; Residues: 1-911 <1002 A; Cross-references: GB:MZ7819; NID:9178215; PIDN:AAA35514.1; PID:9178216 B; Tanner, M.J.A.; Martin, P.G.; High, S. Biochem J. 255, 703-712, 1988 B; Title: The complete amino acid sequence of the human erythrocyte membrane anion-tra A; Reference number: S03074; MUID:89134172; PMID:3223947

A; Accession: S03074

A;Molecule type: mRNA A;Residues: 1-55, E',57-911 <TAN> A;Cross-references: EMBL:X12609; NID:928713; PIDN:CAA31128.1; PID:928714 R;Showe, L.C.; Ballanthe, M.; Huebner, K.

ပ္ပ

```
A25314
band 3 protein - mouse
C;Species: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 20-Aug-1999
C;Accession: A55314, A56086; I49524; B25104
R;Kopito, R.R.; Lodish, H.F.
Nature 316, 234-238, 1985
A;Title: Primary structure and transmembrane orientation of the murine anion exchange
                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: erythrocyte
A;Note: sequence extracted from NCBI backbone (NCBIP:113819, NCBIP:113821, NCBIP:1138
A;Note: a histidine residue exsential for anion transport is suggested to be His-651,
B;Okubo, K.; Kang, D.; Hamasaki, N.; Jennings, M.L.
J. Biol. Chem. 269, 1918-1926, 1994
A;Title: Red blood cell band 3. Lysine 539 and lysine 851 react with the same H-2DIDS
A;Reference number: A49717; MUID:94124538; PMID:8294441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 427-436,479-519;538-540;559-566;809-817;825-841;849-857 <OKU>
A;Note: Lys-539 and Lys-851 were shown to bind the same molecule of the anion transpo
R;Hamasaki, N.; Okubo, K.; Kuma, H.; Kang, D.; Yae, Y.
J. Biochem. 122, 577-585, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Proteolytic cleavage sites of band 3 protein in alkali-treated membranes: Fi
A;Reference number: PC4403; MUID:98006310; PMID:9348087
A;Accession: PC4403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Reywords: acetylated amino end; glycoprotein; ion transport; phosphoprotein; transm F;1-403/Region: cytoskeletal protein binding
                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 361-372;390-399;604-613;632-639;647-656;699-729;731-743;761-781;818-826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Residues: 361-911 <HAM>
C; Comment: Band 3 is the major integral glycoprotein of the erythrocyte membrane. A
C; Comment: Band 3 has at least two functional domains. Its integral domain mediates
ing sites for cytoskeletal proteins, glycolytic enzymes, and hemoglobin.
                                                                     J. Biól. Chem. 267, 19211-19217, 1992
A;Title: A structural study of the membrane domain of band 3 by tryptic digestion.
A;Reference number: A44116; WUID:92406862; PMID:1527044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F,539,590,851/Binding site: anion (Lys) #status experimentur
F,642/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Met) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 104; DB 1; Length 911; 100.0%; Pred. No. 9e-09;
                              Hamasaki, N.; Kuroda, N.; Shiraki, H.
211-19217, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <TM10>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <TM14>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 17q21-17q22
C; Superfamily: band 3 anion transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GDB:119874; OMIM:109270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transmembrane #status
transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1/Modified site: acetylated amino end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              720 GMPWLSATTVRSVTHANALT 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GMPWLSATTVRSVTHANALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anion antiporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: GDB:SLC4A1; EPB3
                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                      A; Accession: A44116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;861-881/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        404-911/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               405-427/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              435-457/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     459-479/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -507/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   604-624/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       659-680/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3-743/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-780/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;785-806/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              839-859/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
Genomics 1, 71-76, 1987

A.Title: Localization of the gene for the erythroid anion exchange protein, band 3 (EMPE A.Reference number: 139408; MUID:88031311; PMID:3478298

A.Accession: 139408

A.Accession: 139409

A.Residues: 37-56 GSH01>
A.Residues: 197-56 GSH01>
A.Residues: 198-10A

A.Residues: 189409

A.Residues: 199404

A.Residues: 199405

A.Residues: 280, 7881-7990

A.Reference number: 390, 1983

A.Title: Amarby

A.Reference number: 39100, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-10, 70, 12-68, E, 69-200 <KAU>
A; Residues: 1-10, 70, 12-68, E, 69-200 <KAU>
B; Brock, C.J.; Tanner, M.J.A.; Kempf, C.
Biochem. J. 213, 577-586, 1983
A; Title: The human erythrocyte anion-transport protein.
A; Reference number: A90323; MUID:83308584; PMID:6615451
A; Accession: A90323
A; Molecule type: protein
A; Residues: 559-630 <ARS hown to bind phenyl isothicoyanate, an inhibitor of anion transport
A; Note: Lys-590 was shown to bind phenyl isothicoyanate, an inhibitor of anion transport
R; Kawano, Y.; Okubo, K.; Tokunaga, F.; Miyata, T.; Iwanaga, S.; Hamasaki, N.
J. Biol. Chem. 263, 8232-8238, 1988
A; Title: Localization of the pyridoxal phosphate binding site at the COOH-terminal regic
A; Reference number: A28079; MUID:88228050; PMID:3372523
A; Molecule type: protein
A; Residues: 834-842, XX, 844-911 <KAW>
A; Molecule type: protein
A; Residues: Baya 842, XX, 844-911 <KAW>
A; Molecule type: protein
A; Residues: Baya 843, X3, 1989
A; Molecule type: protein band 3
A; Reference number: S05523; MUID:90001294; PMID:2790053
A; Reference number: S05523; MUID:90001294; PMID:2790053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 361-364, X', 366-372;424-429, X', 431-434 <COB>
A; Residues: 361-364, X', 366-372;424-429, X', 431-434 <COB>
A; Residues: 361-364, X', 366-372;424-429, X', 431-434 <COB>
B; Note: Lys-430 is labeled by eosinyl-5-maleimide (EMA) in intact erythrocytes
B; Namoukakos, D.; Vasseur, C.; Driancourt, C.; Blouquit, Y.; Delaunay, J.; Wajcman, H.;
Blood 78, 1117-1120, 1991
A; Title: Human erythrocyte band 3 polymorphism (band 3 Memphis): characterization of the A; Reference number: A44933; MUID:91329825; PMID:1678289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 1.201;220-292;307-308, 'R',310-312, 'S',314-329, 'K',331-333;347-370 < YAN1>
R; Cobb, C.E.; Beth, A.H.
Biochemistry 29, 8283-8290, 1990
A; Title: Identification of the eosinyl-5-maleimide reaction site on the human erythrocyt
A; Reference number: A35835; MUID:91070049; PMID:1701324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-55,'E',57-69 <YAN2>
A;Note: sequence extracted from NCBI backbone (NCBIP:49829)
A;Note: sequence of a common polymorphic form designated band 3 Memphis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecule type: protein seasides: 1-10, 10, 12-68, E', 69-200 <KAU>
stacidus: 1-10, 10, 12-68, E', 69-200 <KAU>
Brock, C.J.; Tanner, M.J.A.; Kempf, C.
tochem. J. 213, 577-586, 1983
Title: The human erythrocyte anion-transport protein.
Reference number: A90323; MUID:83308584; PMID:6615451
Accession: A90323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A35835
A; Status: preliminary
```

ö

Gaps

a Q

3

Med Sep

us-10-087-464-1.rpr

```
C;Accession: A30816
R;Kim, H.R.C.; Yew, N.S.; Ansorge, W.; Voss, H.; Schwager, C.; Vennstroem, B.; Zenke, Mol. Cell. Biol. 8, 4416-4424, 1988
A;Titler Two different mRNAs are transcribed from a single genomic locus encoding the A;Reference number: A30816; MUID:89039870; PMID:3185555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Flevet, B.; Gabillat, N.; Borgese, F.; Motais, R.
EMBO J. 14, 5158-5169, 1995
A;Title: Expression of band 3 anion exchanger induces chloride current and taurine tr
A;Reference number: S59861; MUID:96080151; PMID:7489705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem. J. 285, 17-23, 1992
A;Title: Amino acid sequence of band-3 protein from rainbow trout erythrocytes derive
A;Reference number: S24318; MUID:92344566; PMID:1637296
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-912 <FIE>
A; Cross-references: EMBL:250848; NID:g1004316; PIDN:CAA90701.1; PID:g1004317 C; Superfamily: band 3 anion transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    band 3 anion transport protein - rainbow trout
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 20-Aug-1999
C;Accession: S24318; S36083; S22173
R;Huebner, S; Michel, F.; Rudloff, V.; Appelhans, H.
Biochem. J. 285, 17-23, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 20-Aug-1999
  C;Species: Gallus gallus (chicken)
C;Date: 01-Dec-1989 #sequence_revision 30-Sep-1991 #text_change 16-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-304,'G',306-918 <APP>
A;Cross-references: EMBL:X61699; NID:g64308; PIDN:CAA43868.1; PID:g64309
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                     Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Db w,
2.7e-07;
~~ 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 912;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               band 3 anion transport protein isoform b - rainbow trout
                                                                                                                                                                                                                                                                                                                                                                       Score 100; DB 2; L
Pred. No. 4.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 95; DB 2;
Pred. No. 2.7e-07
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, August 1991
                                                                                                                                                                                                                        A Molecule type: mRNA
A;Residues: 1-922 <KIM>
A;Cross-references: GB:M23404
S.Superfamily: band 3 anion transport protein
C;Reywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 71-89;94-114;570-588 <HUE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        731 GMPWLSATTVRTITHANALT 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 96.2%;
Best Local Similarity 90.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 90.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: EMBL:X61699
A; Accession: S36083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: S22173
A; Accession: S22173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-918 <HUE1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S24318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S59861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: S5986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Appelhans, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: MA
A; Molecule type: MA
A; Cross-references: GB-J02756; NID:9192136; PIDN:AAA37278.1; PID:9553874
B; Demuth, D.R.; Showe, L.C.; Ballantine, M.; Palumbo, A.; Fraser, P.J.; Cloe, L.; Rovera
BMBO J: S, 1205-1214, 1986
A; Title: Cloning and structural characterization of a human non-erythroid band 3-11ke pr
A; Reference number: A91039; MUID:86274622; PMID:3015590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: 150159
R;Cox, J.V.; Lazarides, E.
R;Cox, J.V.; Lazarides, E.
A) 137-1335, 1988
A;Title: Alternative primary structures in the transmembrane domain of the chicken eryth A;Reference number: 150159; MUID:88216609; PMID:2835670
A;Accession: 150159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Introns: 5/3; 46/1; 70/3; 131/1; 176/2; 217/3; 245/1; 305/3; 376/1; 447/1; 496/3; 561/
C:Superfamily: band 3 anion transport protein
C:Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M29379; NID:g191741; PIDN:AAA37187.1; PID:g191742 R;Kopito, R.R.; Andersson, M.; Lodish, H.F.
B. Biol. Chem. 262, 8032-8040, 1987
A;Title: Structure and organization of the murine band 3 gene.
A;Reference number: 149524; MUID:87250387; PMID:3036795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M19496; NID:g211211; PIDN:AAA48604.1; PID:g211212
C;Superfamily: band 3 anion transport protein
                                                    A; Molecule type: mRNA
A; Residues: 1-929 < KOP>
A; Cross-references: GB: CACP>
A; Cross-references: GB: CACP>
A; Cross-references: GB: CACP>
A; Cross-references: GB: CACP; NID: G49897; PIDN: CAA26506.1; PID: G49898
B; Kopito, R.R.; Lodish, H.F.
J. Cell. Biochem. 29, 1-17, 1985
A; Title: Structure of the murine anion exchange protein.
A; Reference number: A26086; MUID: 86034211; PMID: 3840489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 11-466,'S',468-929 <DEM>
A;Cross-references: GB:X03917; NID:953042; PIDN:CAA27555.1; PID:953043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A30816
band 3 anion transport protein (clone pBIIIC1) - chicken
A; Reference number: A25314; MUID:85268011; PMID:2410791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 104; DB 2; 100.0%; Pred. No. 9.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 100; DB 2;
Pred. No. 3.7e-08;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96.2%; Score 100; 90.0%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      738 GMPWLSATTVRSVTHANALT 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GMPWLSATTVRSVTHANALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity 90.0
18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anion transporter - chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
es 20; Conserv
                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-929 <KO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1-844 <COX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-844 <CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: I49524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: B25104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C;Accession: S21086
A;Title: Complete nucleotide sequence of band 3 related anion transport protein AE2 f
A;Reference number: S21086; MUID:92223115; PMID:1562608
A;Status: preliminary
                                                                               C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 20-Aug-1999
C;Datession: 317189
R;Alper, S.L.; Kopito, R.R.; Libresco, S.M.; Lodish, H.F.
J; Biol. Chem. 263, 17092-17099, 1988
A;Title: Cloning and characterization of a murine band 3-related cDNA from kidney and A;Reference number: A31789; MUID:89034212; PMID:3182834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein from ileum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Cross-references: GB: S45791; NID: 9256659; PIDN: AAB23488.1; PID: 9256660
A; Experimental source: New Zealand White rabbit, lieal epithelial cells
A; Note: sequence extracted from NCBI backbone (NCBIN:115180, NCBIP:115181)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-1240 <GEH>
A; Cross-references: EMBL:X62137; NID:g28424; PIDN:CAA44067.1; PID:g28425 C; Superfamily: band 3 anion transport protein
                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-1237 (ALLP)
A; Cross-references: GB:J04036; NID:g192132; PIDN:AAA65505.1; PID:g309114
C; Superfamily: band 3 anion transport protein
C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; DB 2; ... 7.8e-07; ... 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C)Accession: A56764
R;Chow, A.; Dobbins, J.W.; Aronson, P.S.; Igarashi, P.
R;Chow, A.; Dobbins, J.W.; Aronson, P.S.; Igarashi, P.
A;Title: CDNA cloning and localization of a band 3-related lakeference number: A56764; MUID:93035730; PMID:1415547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; L
7.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 93; DB;
; Pred. No. 7.8e-
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 93; DB;
Pred. No. 7.8e-
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: band 3 anion transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1046 GLPWLAAATVRSVTHANALT 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    band 3-related protein, ileum - rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.4%;
85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anion exchange protein 2 - human
                                                                        band 3-related protein - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 89.4
Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A56764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
S21086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dailu 3-Teracue protein 2-18 (Norway rat)
C; Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 20-Aug-1999
C; Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 20-Aug-1999
C; Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 20-Aug-1999
C; Accession: A34911, A35770
A; Title: coNA cloning and tissue distribution of mRNAs for two proteins that are related A; Reference number: A34911, MUD: 90094439; PMID: 2294114
A; Reference number: A34911, MUD: 90094439; PMID: 2294114
A; Reference number: A34911, MUD: 90094439; PMID: 2294114
A; Residues: 1-1234 «KUD>
A; Reference number: A35770; MUD: 90319095; PMID: 2371270
A; Reference number: A35770; MUD: 90319095; PMID: 2371270
A; Status: preliminary: nucleic acid sequence not shown; not compared with conceptual trativolues: 1-205, A, 207-924, PG', 927-1017, IV', 1020-1155, ID', 1158-1234 «LIN>
C; Superfamily: band 3 anion transport protein
C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
C.Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
C.Date: 10-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
C.Date: 10-Nov-1988 #sequence_revision 10-Nov-1988 #text_change 20-Aug-1999
C.Date: 10-Nov-1988 #sequence_revision 10-Nov-1988 #text_change 20-Aug-1999
E.Date: 10-Nov-1988 #sequence_revision 10-Nov-1988 #text_change 20-Aug-1999
C.Date: 10-Nov-1988 #text_change 20-Aug-1999
C.Nov-1988 #text_change 20-Aug-1999
C.Date: 10-Nov-1988 #text_change 20-Aug-1999
C.Date: 10-Nov-1998 #text_change 20-Aug-1999
C.Date: 10-Nov-1998 #text_change 20-Aug-1999
C.Date: 10-Nov-1999
C.Date: 10-Nov-1999
C.Date: 10-Nov-1999
C.Date: 10-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 93; DB 2; Length 1234;
Pred. No. 7.8e-07;
2; Mismatches 1; Indels
                                                                                                       Length 918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 93; DB 2; Length vo...
Pred. No. 5.3e-07;
                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 protein, nonerythroid (MEB3) - human (fragment)
                                                                                                    Score 95; DB 2; Pred. No. 2.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                     1; Mismatches
C;Superfamily: band 3 anion transport protein C;Keywords: erythrocyte; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1043 GLPWLAAATVRSVTHANALT 1062
                                                                                                                                                                                                                                                                      674 GLPWLAAATVRSVTHANALT 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                       1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.4%;
ilarity 85.0%;
Conservative
                                                                                                    91.3%;
90.0%;
                                                                                             Query Match
Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3-related protein 2 - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S:
Matches 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                 A25104
band 3
                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
```

ö

```
1037 GLPWLTAATVRSVTHVNALT 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                completed: September
ne : 18.25 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1030 < LINI>
A;Cross-references: GB:M87060; NID:g202770
A;Note: this translation is not annotated in GenBank entry RATAE3A, release 111.0; this A;Note: sequence extracted from NCBI backbone (NCBIN:96971, NCBIP:96975)
A;Notecsion: B42497
A;Notecule type: DNA
A;Residues: 1-73, E' <IIN2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rilinn, S.C.; Kudrycki, K.E.; Shull, G.E.
J. Biol. Chem. 267, 7927-7935, 1992
A;Title: The predicted translation product of a cardiac AE3 mRNA contains an N terminus gene, and identification of an alternative transcription initiation site.
A;Reference number: A42497; MUID:92218461; PMID:1560021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Cross-references: GB:M87060; NID:g202770; PIDN:AAA40692.1; PID:g202771
A,Experimental source: tissue type spleen
C,Superfamily: band 3 anion transport protein
C,Keywords: alternative splicing; cardiac muscle; heart; transmembrane protein
                                                                                                                                                                                                                                     anion exchanger 3, cardiac splice form - rat
N;Alternate names: AE3; chloride/bicarbonate exchanger 3
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 07-Dec-1999
C;Accession: A42497; B42497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-1277 <KUD)
A; Cross-references: GB:J05167; NID:g203088; PIDN:AAA40798.1; PID:g203089
C; Superfamily: Dand 3 anion transport protein
C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 89; DB 2; Length 1030;
Pred. No. 2.9e-06;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 89; DB 2; Length 122
Pred. No. 3.5e-06;
2; Mismatches 2; Indels
                                     Indels
85.0%; Pred. No. 7.9e-07;
                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1037 GLPWLTAATVRSVTHVNALT 1056
                                                                                                          1049 GLPWLAAATVRSVTHANALT 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GMPWLSATTVRSVTHANALT 20
                                                                                 1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 80.0%; Promatches 16; Conservative 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.6%;
80.0%;
            Best Local Similarity 85.0% Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 85.69
Best Local Similarity 80.09
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  band 3-related protein 3 - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: B34911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                    ò
                                                                                                                                q
```

RESULT 15 A33638

```
erythrocyte anion exchanger homolog AE3 - mouse
C; Species: Mus musculus (house mouse)
C; Date: 02-Feb-1990 #sequence_revision 02-Feb-1990 #text_change 20-Aug-1999
C; Accession: A33698
E; Kopito, R.R.; Lee, B.S.; Simmons, D.M.; Lindsey, A.E.; Morgans, C.W.; Schneider, K. Cell 59, 927-937, 1989
A; Title: Regulation of intracellular pH by a neuronal homolog of the erythrocyte anio A; Reference number: A33638; MUID:90075236; PMID:2686841
A; Recession: A33638
A; Status: preliminary
A; Molecule type: mRNA
A; Recences: GB:M28383; NID:9191735; PIDN:AAA37184.1; PID:9309095
C; Superfamily: band 3 anion transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 89; DB 2; 1
Pred. No. 3.5e-06;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                         85.68;
80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 80.0
Matches 16; Conservative
```

3, 2003, 11:51:16

THIS PAGE BLANK (USPTO)

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

112 1 DRILLEFKPPKYHPDVPYVK 20 US-10-087-464-4 Title: Perfect score: Sednence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	*			SUMMARIES	
Score	Match	Length DB	DB	ID	Description
12	100.0	911	Н	взни	band 3 anion trans
108	96.4	848	7	A33810	band 3 anion trans
108	96.4	929	7	A25314	band 3 protein - m
82	73.2	844	7	150159	anion transporter
82	73.2	922	7	A30816 ·	band 3 anion trans
74	66.1	865	7	A25104	
74	66.1	1234	7	A34911	band 3-related pro
74	66.1	1237	7	A31789	band 3-related pro
74	66.1	1237	~	A56764	band 3-related pro
74	66.1	1240	~	S21086	anion exchange pro
68	60.7	1030	7	A42497	anion exchanger 3,
89	60.7	1227	7	B34911	band 3-related pro
89	60.7		7	A33638	erythrocyte anion
99	58.9		~	T37460	probable sodium bi
99	58.9	1175	7	T22491	hypothetical prote
63	56.2		~	T31336	sodium bicarbonate
62	55.4	-	7	I38496	anion exchanger 3
20	44.6	468	Н	B84540	acid phosphatase (
20	44.6		7	S59861	
20	44.6		~	S24318	band 3 anion trans
49	43.8		Н	QQBE40	BGLF2 protein - hu
49	43.8		-	H84669	acid phosphatase (
49	43.8		Н	A59200	acid phosphatase (
49	43.8	Н	7	PC7034	Na+ bicarbonate co
48	42.9		7	B75095	probable histone d
48	42.9		-	H71071	hypothetical prote
48	42.9		7	T43810	methylaspartate am
48	42.9		7	C96940	sporulation specif
48	42.9	П	7	T13962	sodium bicarbonate

sodium bicarbonate sodium bicarbonate	conserved hypothet transqlutaminase t	acid phosphatase (hypothetical prote	hypothetical prote	replicative DNA he	hypothetical prote	hypothetical prote	alpha 2,6-sialyltr	beta-galactoside a	beta-galactoside a	acid phosphatase (nodule-specific hy
T14110 T14031	F69019 B84146	T04599	T30143	E72237	G82329	T23748	AH1642	C42327	A28451	A41734	A59201	S11967
2 2	7 7	٦.	1 73	7	7	7	7	7	7	7	7	7
1035 1079	234	466	137	306	468	1156	77	214	403	406	431	434
42.9	42.0	42.0	41.1	41.1	41.1	41.1	40.6	40.2	40.2	40.2	40.2	40.2
48 48	47	47	46	46	46	46	45.5	45	45	45	45	45
30 31	32 33	34	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	ALCOUR I
	B3HU
	band 3 anion transport protein, erythrocyte - human
	N;Alternate names: carrier family 4, anion exchanger, member 1; erythroid anion excha
	C;Species: Homo sapiens (man)
_	C;Date: 03-Aug-1984 #sequence_revision 03-Oct-1995 #text_change 22-Jun-1999
	C; Accession: A36218; S03074; I39408; I39409; A92237; A26507; A92430; A90323; A28079;
_	R; Lux, S.E.; John, K.M.; Kopito, R.R.; Lodish, H.F.
	Proc. Natl. Acad. Sci. U.S.A. 86, 9089-9093, 1989
	A; Title: Cloning and characterization of band 3, the human erythrocyte anion-exchange
_	A; Reference number: A36218; MUID:90083213; PMID:2594752
	A; Accession: A36218
	A;Status: preliminary
	A; Molecule type: mRNA
	A; Residues: 1-911 <lux></lux>
	A; Cross-references: GB: M27819; NID: 9178215; PIDN: AAA35514.1; PID: 9178216
_	R;Tanner, M.J.A.; Martin, P.G.; High, S.
	Biochem. J. 256, 703-712, 1988
	A; Title: The complete amino acid sequence of the human erythrocyte membrane anion-tra
	A; Reference number: S03074; MUID:89134172; PMID:3223947
_	A; Accession: S03074
	A; Molecule type: mRNA

A, Residues: 1-55, E', 57-911 <TAN>
B, Schowe, L.C.; Ballantine, M.; Huebner, K.
Genomics 1, 71-76, 1987
A, 711-11e: Localization of the gene for the erythroid anion exchange protein, band 3 (B A, Reference number: 139408; MUID:88031311; PMID:3478298

A; Molecule type: DNA
A; Residues: 37-56 <SHOl>
A; Residues: 37-56 <SHOl>
A; Cross-references: GB:MI6978; NID:g178217; PIDN:AAA51670.1; PID:g178220
A; Accession: 139409
A; Molecule type: DNA
A; Residues: 118-161 <SHO2>
A; Residues: 118-161 <SHO2>
B; Cross-references: GB:MI6979; NID:g178218; PIDN:AAA51671.1; PID:g553169

A, Disol. Chem. 253, 7242-7248, 1978
A,Tille: Orientation of the band 3 polypeptide from human erythrocyte membranes. Iden A, Reference number: A92237; MUID:79027186; PMID:701248
A, Rocession: A92237; MUID:79027186; PMID:701248
A, Rocession: A92237; MUID:79027186; PMID:701248
A, Rocession: A, Molecule type: protein
A, Rocelle type: protein
A, Rocelle type: Protein
B, Mawby, W. J.; Findlay, J. B. C.
Biochem. J. 205, 465-475, 1982
A,Tille: Characterization and partial sequence of di-iodosulphophenyl isothiocyanate-A, Reference number: A26507; MUID:83074521; PMID:7150226

A, Accession: A26507 A; Molecule type: protein A; Residues: 437-473; 360-364,'D',366-369 <MAW> R; Raul, R.K.; Murthy, S.N.P.; Reddy, A.G.; Steck, T.L.; Kohler, H. J. Biol. Chem. 258, 7981-7990, 1983

ø

```
A33810
band 3 anion transport protein - rat
C;Species: Rattus norvegious (Norway rat)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 20-Aug-1999
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 20-Aug-1999
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 20-Aug-1999
C;Accession: 264, 8185-8192, 1989
A;Title: Primary structure of the rat kidney band 3 anion exchange protein deduced fr
A;Reference number: A33810; MUID:89255254; PMID:2722777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dand 3 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-011-1987 *Requence_revision 22-Jul-1987 *text_change 20-Aug-1999
C;Accession: A25314; A26086; I49524; B25104
R;Kopito, R.R.; Lodish, H.F.
Nature 316, 234-238, 1985
A;Title: Primary structure and transmembrane orientation of the murine anion exchange
                                                                                                                                                 A; Map position: 17q21-17q22
C; Superfanily: band 3 anion transport protein
C; Keywords: acetylated amino end; glycoprotein; ion transport; phosphoprotein; transm
F:1-403/Region: cytoskeletal protein binding
                  C;Comment: Band 3 has at least two functional domains. Its integral domain mediates ing sites for cytoskeletal proteins, glycolytic enzymes, and hemoglobin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB:J04793; NID:g203092; PIDN:AAA40800.1; PID:g203093 C; Superfamily: band 3 anion transport protein C; Keywords: alternative splicing; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F:1/Modified site: acetylated amino end (Met) #status experimental F:539,590,851/Binding site: anion (Lys) #status experimental F:642/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                         <TM05>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <TM08>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <TM10>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <TM11>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <TM12>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <TM13>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 112; DB 1;
100.0%; Pred. No. 5.5e-09;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 108; DB 2;
Pred. No. 2.1e-08;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                 predicted
                                                                                                                                                                                                                                                                                                                                                                                         predicted
                                                                                                                                                                                                                                                                                                                                                                                                                    predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                            predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        predicted
predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      predicted
                                                                                                                         A; Cross-references: GDB:119874; OMIM:109270
                                                                                                                                                                                                                                                                                     transmembrane #status
                                                                                                                                                                                                                                                                                                                                      transmembrane #status
transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                         transmembrane #status
                                                                                                                                                                                                                                                                                                                transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                    transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                            transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transmembrane #status
transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DRILLERKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DRILLLEKPPKYHPDVPYVK
                                                                                                                                                                                                                                                             anion antiporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             larity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                 A; Gene: GDB:SLC4A1; EPB3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
tes 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-848 <KUD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;659-680/Domain: E;701-721/Domain: E;723-743/Domain: E;764-780/Domain: E;785-806/Domain: E;835-885/Domain: E;861-881/Domain: E;
                                                                                                                                                                                                                                                     F;404-911/Region:
F;405-427/Domain:
                                                                                                                                                                                                                                                                                                                                   F;459-479/Domain:
F;491-507/Domain:
                                                                                                                                                                                                                                                                                                              435-457/Domain:
                                                                                                                                                                                                                                                                                                                                                                                      522-542/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                               568-588/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                          604-624/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
Any Title : Mindon caid sequence of the Nullpha) terminal 301 residues of human erythrocyte Anderseanon number: 10, 107.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 10.210, 1
```

ö

Gaps

ö

ö

Gaps

ö

```
Chacession: A30816
R.Kim, H.R.C.; Yew, N.S.; Ansorge, W.; Voss, H.; Schwager, C.; Vennstroem, B.; Zenke, Mol. Biol. 8, 4416-4424, 1988
Mol. Cell. Biol. 8, 4416-4424, 1988
A.Title: Two different mRNAs are transcribed from a single genomic locus encoding the A; Reference number: A30816; MUID:89039870; PMID:3185555
A.Accession: A30816
A.Molecule type: mRNA
A; Residues: 1-922 < KINA
A; Residues: 1-922 < KINA
A; Residues: GB:M23404
C; Superfamilly: band 3 anion transport protein
C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: A25104

R;Demuth, D.R.; Showe, L.C.; Ballantine, M.; Palumbo, A.; Fraser, P.J.; Cioe, L.; Rov EMBO J. 5, 1205-1214, 1986

A;Title: Cloning and structural characterization of a human non-erythroid band 3-like A;Reference number: A91039; MUID:86274622; PMID:3015590

A;Recession: A55104

A;Residues: 1-865 < DEM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 20-Aug-1999
C;Accession: A34911; A35770
R;Kudrycki, K.E.; Newman, P.R.; Shull, G.E.
J. Biol. Chem. 265, 462-471, 1990
A;Title: CDNA cloning and tissue distribution of mRNAs for two proteins that are rela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNÅ
A; Residues: 1-1214 < (MLD)
A; Cross-references: GB:J05166; NID:g203090; PIDN:AAA40799.1; PID:g203091
A; Lindsey, A.E.; Schneider, K.; Simmons, D.M.; Baron, R.; Lee, B.S.; Kopito, R.R.
Proc. Natl. Acad. SGI. U.S.A. 87, 5278-5282, 1990
A; Title: Functional expression and subcellular localization of an anion exchanger clo
A; Reference number: A35770; MUID:90319095; PMID:2371270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: A33570
A; Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-205, 'A', 207-924,'PG', 927-1017,'IV', 1020-1155,'ID', 1158-1234 <LIN>
C; Superfamily: band 3 anion transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
                                  C;Date: 01-Dec-1989 #sequence_revision 30-Sep-1991 #text_change 16-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A)Cross-references: GB:X03918; NID:g32120; PIDN:CAA27556.1; PID:g32121
C;Superfamily: band 3 anion transport protein
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 74; DB 2; Length 865
Pred. No. 0.0034;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A25104
band 3 protein, nonerythroid (MEB3) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 73.2%; Score 82; DB 2; Local Similarity 78.9%; Pred. No. 0.00022; les 15; Conservative 0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :|: || ||:||| |||
761 ERLHLLLMPPKHHPDVTYVK 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       818 DRILLLLMPPKYHPKEPYV 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DRILLERKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DRILLEKPPKYHPDVPYV 19
   gallus (chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 66.1%;
Best Local Similarity 65.0%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                band 3-related protein 2 - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: A34911
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 4-70', X', 709-902 <RES>
A;Cross-references: 6B:J02756; NID:9192136; PIDN:AAA37278.1; PID:9553874
A;Cross-references: GB:J02756; NID:9192136; PIDN:AAA37278.1; PID:9553874
B;Demuth, D.R.; Showe, L.C.; Ballantine, M.; Palumbo, A.; Fraser, P.J.; Cioe, L.; Rovera
EMBO J. 5, 1205-1214, 1986
A;Title: Cloning and structural characterization of a human non-erythroid band 3-like pr
A;Reference number: A91039; MUID:86274622; PMID:3015590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anion transporter - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Aug-1999
C;Cosesion: 150159
R;Cox, J.V.; Lazarides, E.
Mol. Cell. Biol. 8, 1377-1335, 1988
Mol. Cell. Biol. 8, 1377-1335, 1988
A;Title: Alternative primary structures in the transmembrane domain of the chicken eryth
A;Reference number: 150159; MUID:88216609; PMID:2835670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Introns: 5/3; 46/1; 70/3; 131/1; 176/2; 217/3; 245/1; 305/3; 376/1; 447/1; 496/3; 561/
C;Superfamily: band 3 anion transport protein
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-929 <KO2>
A; Residues: 1-929 <KO2>
A; Cross-references: GB:NQ379; NID:g191741; PIDN:AAA37187.1; PID:g191742
B; Kropito, R.R.; Andersson, M.; Lodish, H.F.
J. Biol. Chem. 262, 8035-8040, 1987
A; Title: Structure and organization of the murine band 3 gene.
A; Reference number: 149524; MUID:87250387; PMID:3036795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-844 <COX>
A; Cross-references: GB:M19496; NID:g211211; PIDN:AAA48604.1; PID:g211212
C; Superfamily: band 3 anion transport protein
                           A; Accession: A25314
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-929 CKOP>
A; Cross-references: GB: X02677; NID: g49897; PIDN: CAA26506.1; PID: g49898
R; Kopito, R.R.; Lodish, H.F.
C. Cell. Biochem. 29, 1-17, 1985
A; Title: Structure of the murine anion exchange protein.
A; Reference number: A26086; MUID: 86034211; PMID: 3840489
A; Accession: A26086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 11-466,'S', 468-929 <DEM>
A;Cross-references: GB:X03917; NID:953042; PIDN:CAA27555.1; PID:953043
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 96.4%; Score 108; DB 2; Length 929; Best Local Similarity 95.0%; Pred. No. 2.3e-08; Matches 19; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , DB 2; Leus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
A30816
band 3 anion transport protein (clone pBIIIC1) - chicken
A; Reference number: A25314; MUID:85268011; PMID:2410791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 82; DB 2
Pred. No. 0.000
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DRILLLFKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  740 DRILLLLMPPKYHPKEPYV 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DRILLERPPKYHPDVPYV 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 73.2%;
Best Local Similarity 78.9%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: I49524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
```

Gaps

ö

Ω

ð

```
C;Accession: B34911
R;Kudrycki, K.E.; Newman, P.R.; Shull, G.E.
A; Biol. Chem. 265, 462-471, 1990
A;Title: cDNA cloning and tissue distribution of mRNAs for two proteins that are rela A;Reference number: A34911; MUID:90094439; PMID:2294114
A;Accession: B34911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rilin, S.C.; Kudrycki, K.E.; Shull, G.E. J. Biol. Chem. 267, 7927-7935, 1992
A; Title: The predicted translation product of a cardiac AE3 mRNA contains an N termin gene, and identification of an alternative transcription initiation site.
A; Reference number: A42497; MUID:92218461; PMID:1560021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-1030 <LINI>
A;Cross-references: GB:M87060; NID:g202770
A;Orce: this translation is not annotated in GenBank entry RATAE3A, release 111.0; th
A;Note: sequence extracted from NCBI backbone (NCBIN:96971, NCBIP:96975)
Complete nucleotide sequence of band 3 related anion transport protein AE2 nce number: $21086; MUID:92223115; PMID:1562608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:M87060; NID:g202770; PIDN:AAA40692.1; PID:g202771
A;Experimental source: tissue type spleen
C;Superfamily: band 3 andon transport protein
C;Keywords: alternative splicing; cardiac muscle; heart; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anion exchanger 3, cardiac splice form - rat
N;Alternate names: AE3; Chloride/Dicarbonate exchanger 3
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Oct-1999 *sequence_revision 29-Oct-1999 *text_change 07-Dec-1999
C;Accession: A42497; B42497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         band 3-related protein 3 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:J05167; NID:g203088; PIDN:AAA40798.1; PID:g203089 C;Superfamily: band 3 anion transport protein C;Keywords: transmembrane protein
                                                                                                                                                                                                           A;Cross-references: EMBL:X62137; NID:928424; PIDN:CAA44067.1; PID:928425 C;Superfamily: band 3 anion transport protein C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                    Length 1240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: Indels
                                                                                                                                                                                                                                                                                                                                                 DB 2;
0.005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
0.034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                 Score 74; DB 2
Pred. No. 0.005
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 68;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :|: || |||:||| |||
1136 ERLHLLLMPPKHHPDVTYVK 1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DRILLLFKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:||:| | |:||: |||
928 RLLLIFMPAKHHPEQPYV 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 RILLEKPPKYHPDVPYV 19
                                                                                                                                                                                                                                                                                                                                                    66.1%;
65.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.7%;
61.1%;
                                                                                                                                                                                                                                                                                                                                                    Query Match 66.1's
Best Local Similarity 65.0
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <LIN2>
                                                                                                     A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-1240 <GEH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-1227 <KUD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA A; Residues: 1-73, 'E'
                                       A; Reference number:
                                                                    A; Accession: S21086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: B42497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                               Dand 3-related protein - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 20-Aug-1999
C; Accession: A31789
R; Alper, S.L.; Kopito, R.R.; Libresco, S.M.; Lodish, H.F.
J. Biol. Chem. 263, 17092-17099, 1988
A; Aitle: Cloning and characterization of a murine band 3-related cDNA from kidney and fr. A; Reference number: A31789; MUD:89034212; PMID:3182834
A; Accession: A31789
A; Accession: A31789
A; Residues: 1-1237 < ALP>
A; Residues: 1-1237 < ALP>
A; Residues: 1-1237 < ALP>
A; Cross-references: GB:304036; NID:g192132; PIDN:AAA65505.1; PID:g309114
C; Superfamily: band 3 anion transport protein
C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                band 3-related protein, ileum - rabbit band 3-related protein, ileum - rabbit band 3-related protein, ileum - rabbit c. Species: Oryctolagus cuniculus (domestic rabbit) c. Species: O. Sp
                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               $21086
anion exchange protein 2 - human
c;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C;Accession: $21086
R;Gehrig, H.; Mueller, W.; Appelhans, H.
Biochim. Biophys. Acta 1130, 326-328, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                        Length 1234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.1%; Score 74; DB 2; Length 1237; llarity 65.0%; Pred. No. 0.005; Conservative 3; Mismatches 4; Indels
                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                        DB 2;
0.005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.1%; Score 74; DB 2;
ilarity 65.0%; Pred. No. 0.005;
Conservative 3; Mismatches
                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                    Score 74;
Pred. No. 0
                                                                                                                                                                                                                                                      1130 ERLHLLLEMPPKHHPDVTYVK 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :|: || |||:|||| |||
1133 ERLHLLLMPPKHHPDVTYVK 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :1: || |||:|||| |||
1133 ERLHLLLMPPKHHPDVTYVK 1152
                                                                                                                                                                                                              1 DRILLLEKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DRILLLFKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DRILLLFKPPKYHPDVPYVK 20
   C; Keywords: transmembrane protein
                                                                        66.1%;
65.0%;
                                                                                                                                             13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
es 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 13; Conserv
                                                                                                            Similarity
                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                            Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
```

g

à

g

ö

Gaps

ö

ô

Gaps

ö

Length 1175; Indels

```
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Roleduel type: DNA
A:Residues: 1-1175 < WILL>
A:Cross-references: EMBL:Z75541; PIDN:CAA99853.1; GSPDB:GN00019; CESP:F52B5.1
A:Experimental source: clone F52B5
C:Genetics: CESP:F52B5.1
                                                                                                                                                                                                                                                                                                                               A;Introns: 67/1; 156/1; 190/3; 253/3; 636/1; 757/3; 977/3; 1021/3; 1139/3 C;Superfamily: band 3 anion transport protein
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 58.9%; Score 66; DB 2; Best Local Similarity 60.0%; Pred. No. 0.079; Matches 12; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: September 3, 2003, 11:51:20
Job time : 18.25 secs
                         submitted to the EMBL Data Library, June 1996 A; Reference number: 219570 A; Accession: T22491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        921 DRILLLEMPMKYQPDTIYIR 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DRILLLFKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                           A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: T37460
R;Romero, M.F.; Boron, W.F.
submitted to the EMBL Data Library, May 1997
A;Description: Identification of a C. elegans protein similar to the electrogenic Na/HCC
A;Reference number: 221700
A;Accession: T37460
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                    erythrocyte anion exchanger homolog AE3 - mouse
C; Species: Mus musculus (house mouse)
C; Date: O2.Feb-1990 #sequence_revision 02-Feb-1990 #text_change 20-Aug-1999
C; Accession: A3538
R; Ropito, R.R.; Lee, B.S.; Simmons, D.M.; Lindsey, A.E.; Morgans, C.W.; Schneider, K.
Cell 59, 927-937, 1989
A; Title: Regulation of intracellular PH by a neuronal homolog of the erythrocyte anion A; Reference number: A33638, MUID:90075236; PMID:2686841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Description: mediates the transport of one Na(+) with multiple HCO3(-) ions C;Superfamily: band 3 anion transport protein C;Keywords: ion transport; transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable sodium bicarbonate cotransport protein NBC - Caenorhabditis elegans N;Alternate names: HCO3 transporter C;Species: Caenorhabditis elegans C;Date: 03-Dec:1999 #sequence_revision 03-Dec-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein F52B5.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 04-Mar-2000
C;Accession: T22491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M28383; NID:q191735; PIDN:AAA37184.1; PID:g309095 C;Superfamily: band 3 anion transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
  Score 68; DB 2; Length 1227; Pred. No. 0.041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 66; DB 2; Length 1119;
Pred. No. 0.075;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1227
                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 68; DB 2;
Pred. No. 0.041;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:AF004926; PIDN:AAC16758.1
C;Genetics:
                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1125 RLLIFMPAKHHPEQPYV 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DRILLEKPPKYHPDVPYVK 20
                                                                                                              2 RILLEFKPPKYHPDVPYV 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 RILLLFKPPKYHPDVPYV 19
Query Match 60.7%;
Best Local Similarity 61.1%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 58.9%;
Best Local Similarity 60.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 60.7%;
Best Local Similarity 61.1%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1227 <KOP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-1119 <ROM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δλ
```

THIS PAGE BLANK (USPTO)

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

September 3, 2003, 11:41:03 ; Search time 17.25 Seconds
(without alignments)
111.500 Million cell updates/sec Run on:

US-10-087-464-2 98 1 SVTHANALIVMGKASTPGAA 20 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283308 Total number of hits satisfying chosen parameters:

283308 segs, 96168682 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		dР			· SUMMARIES	
Result No.	Score	Query	Length	DB	ID	Description
п	86	100.0	911	-	взно	band 3 anion trans
7	91	92.9	848	~	A33810	band 3 anion trans
e	91	92.9	929	7	A25314	e
4	73	74.5	865	7	A25104	band 3 protein, no
2	73	74.5	1234	~	A34911	3-
9	73	74.5	1237	~	A31789	
7	73	74.5	1237	~	A56764	band 3-related pro
80	73	74.5	1240	7	S21086	anion exchange pro
6	7.1	72.4	844	~	I50159	
10	71	72.4	922	7	A30816	band 3 anion trans
11	63	64.3		7	S59861	band 3 anion trans
12	63	64.3		7	S24318	band 3 anion trans
13	19	62.2		~	A42497	anion exchanger 3,
14	61	62.2		~	B34911	band 3-related pro
15	61	62.2		~	A33638	erythrocyte anion
16	61	62.2		7	I38496	anion exchanger 3
17	57	58.2		~	S31828	band 3 anion trans
18	49	50.0	262	~	164139	hypothetical prote
19	48	49.0		~	E97835	hypothetical prote
20	47.5	48.5		7	н95911	probable ferredoxi
21	47	48.0	1300	~	S07575	outer membrane pro
22	45	45.9	1127	7	T28435	proline dehydrogen
23	44	44.9	407	7	T30585	transferase homolo
24	42.5	43.4	707	7	A35804	nucleolin - human
25	42	42.9	303	7	B71638	cell division prot
56	42		343	7	E95911	probable transcrip
27	42	٠	422	7	T09120	basic leucine zipp
28	42	42.9	1213	7	T19835	hypothetical prote
29	42	42.9	1616	~	T47801	

polyketide synthas hypothetical prote	orfl 5' to fcc - S	triosephosphate is	geranylgeranyl dip	ABC transporter, s	probable solute-bi	probable nucleic a	probable RTX famil	hypothetical prote	latent transformin	translation initia	hypothetical prote	hypothetical prote	methionine aminope
T17409 T12541	A44238	F97555	C75400	AG2724	C97506	H75272	B85547	F90696	A55494	AE3544	A82459	T37094	B87106
0.0	01 0	4 (7	7	~	~	7	7	7	7	7	7	~	7
4613 430	122	256	329	497	509	603	5188	5291	1820	128	144	206	285
42.9	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.3	40.8	40.8	40.8	40.8
42	44	4 1	41	41	41	41	41	41	40.5	40	40	40	40
30 31	32	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 R3HI
band 3 anion transport protein, erythrocyte - human
N; Alternate names: carrier family 4, anion exchanger, member 1; erythroid anion excha
C;Species: Homo sapiens (man)
C;Date: 03-Aug-1984 #sequence_revision 03-Oct-1995 #text_change 22-Jun-1999
C; Accession: A36218; S03074; I39408; I39409; A92237; A26507; A92430; A90323; A28079;
R; Lux, S.E.; John, K.M.; Kopito, R.R.; Lodish, H.F.
Proc. Natl. Acad. Sci. U.S.A. 86, 9089-9093, 1989
A; Title: Cloning and characterization of band 3, the human erythrocyte anion-exchange
A; Reference number: A36218; MUID: 90083213; PMID: 2594752
A;Accession: A36218
A;Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-911 <lux></lux>
A, Cross-references: GB: M27819; NID: 9178215; PIDN: AAA35514.1; PID: 9178216
R; Tanner, M.J.A.; Martin, P.G.; High, S.
Biochem. J. 256, 703-712, 1988
A, Title: The complete amino acid sequence of the human erythrocyte membrane anion-tra
A; Reference number: S03074; MUID:89134172; PMID:3223947
A;Accession: S03074
A; Molecule type: mRNA
A, Residues: 1-55, 'E', 57-911 <tan></tan>
A, Cross-references: EMBL: X12609; NID: 928713; PIDN: CAA31128.1; PID: 928714
R;Showe, L.C.; Ballantine, M.; Huebner, K.
Genomics 1, 71-76, 1987
A, Title: Localization of the gene for the erythroid anion exchange protein, band 3 (F

A; Reference number: 139408; MUID:88031311; PMID:3478298 A; Accession: 139408

Appleaule type: DNA
A; Residues: 37-56 <SHO1>
A; Residues: 37-56 <SHO1>
A; Residues: 37-56 <SHO1>
A; Cross-references: GB:M16978; NID:g178217; PIDN:AAA51670.1; PID:g178220
A; Accession: 139409
A; Molecule type: DNA
A; Residues: 118-161 <SHO2>
A; Residues: 118-161 <SHO2>
A; Residues: 118-161 <SHO2>
A; Cross-references: GB:M16979; NID:g178218; PIDN:AAA51671.1; PID:g553169
B; Drickamer, L.K.
J Biol. Chem. 253, 7242-7248, 1978
A; Title: Orientation of the band 3 polypeptide from human erythrocyte membranes. Iden
A; Reference number: A92237; MUID:79027186; PMID:701248
A; Molecule type: Drotein
A; Residues: 1-3 <CHSI
A; Residues: 1-3 <CHSI
A; Residues: 1-3 <CHSI
A; Reference number: A26507; MUID:83074521; PMID:7150226
A; Reference number: A26507; MUID:83074521; PMID:7150226
A; Residues: A37-473;360-364, 'D', 366-369 <AMW>
B; Residues: 437-473;360-364, 'D', 356-369 <AMW>
B; Residues: 437-473;360-364, 'D', 356-369 <AMW>
B; Raul, R.K.; Murthy, S. N.P.; Reddy, A.G.; Steck, T.L.; Kohler, H.
J. Biol. Chem. 258, 7981-7990, 1983

```
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 20-Aug-1999
C;Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 20-Aug-1999
C;Accession: A50514; A50686; I49524; B25104
R;Kopito, R.R.; Lodish, H.F.
Nature 316, 234-238, 1985
A;Title: Primary structure and transmembrane orientation of the murine anion exchange
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RjKudrycki, K.E.; Shull, G.E.
J. Biol. Chem. 264, 8185-8132, 1989
A;Title: Primary structure of the rat kidney band 3 anion exchange protein deduced fr
A;Reference number: A33810; MUID:89255254; PMID:2722777
                                                                                                                                                                                                                                                                                                                        C.Keywords: acetylated amino end; glycoprotein; ion transport; phosphoprotein; transm
F:7-403/Region: cytoskeletal protein binding
             C;Comment: Band 3 has at least two functional domains. Its integral domain mediates ing sites for cytoskeletal proteins, glycolytic enzymes, and hemoglobin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-848 <KUD>
A;Cross-references: GB:J04793; NID:g203092; PIDN:AAA40800.1; PID:g203093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;642/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Met) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 98; DB 1; Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #status experimenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: band 3 anion transport protein C;Keywords: alternative splicing; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 91; DB 2; 1
Pred. No. 6.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 redicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            redicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     redicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                 A;Cross-references: GDB:119874; OMIM:109270
A;Map position: 17q21-17q22
C;Superfamily: band 3 anion transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 91;
                                                                                                                                                                                            GDB:119874; OMIM:109270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;1/Modified site: acetylated amino end F;539,590,851/Binding site: anion (Lys)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVTHANALTVMGKASTPGAA 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVTHANALTVMGKASGPGAA 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SVTHANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SVTHANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A33810
band 3 anion transport protein - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                     F;404-911/Region: anion antiporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.9%;
95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                   A; Gene: GDB: SLC4A1; EPB3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     band 3 protein - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: A33810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A33810
                                                                                                                                                                                                                                                                                                                                                                                                                                                              F:405-427/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;435-457/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F:459-479/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :491-507/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;522-542/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F; 568-588/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;659-680/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .-721/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;723-743/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .64-780/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F; 785-806/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;839-859/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               861-881/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Molecule type: protein
A; Residues: 361-7273:390-399; 604-613; 632-639; 647-656; 699-729; 731-743; 761-781; 818-826 < KAN
A; Residues: 361-7273:390-399; 604-613; 632-639; 647-656; 699-729; 731-743; 761-781; 818-826 < KAN
A; Residuental source: erythrocyte
A; Note: sequence extracted from NCBI backbone (NCBIP:113819, NCBIP:113821, NCBIP:113823,
A; Note: a histidine residue essential for anion transport is suggested to be His-651, Hi
B; Okubo, K.; Kang, D.; Hamasaki, N.; Jennings, M.L.
J. Biol. Chem. 269, 1918-1926, 1994
A; Title: Red blood cell band 3. Lysine 539 and lysine 851 react with the same H-2DIDS (4
A; Reference number: A49717; MUID:94124538; PMID:8294441
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein

A; Molecule type: protein

A; Residues: 559-630 < CRNO

A; Notes: Lys-590 was shown to bind phenyl isothiocyanate, an inhibitor of anion transport

B; Rawano, Y.; Okubo, K.; Tokunaga, F.; Miyata, T.; Iwanaga, S.; Hamasaki, N.

B, B, Lol. Chem. 263, 8232-8238, 1988

A; Title: Localization of the pyridoxal phosphate binding site at the COOH-terminal regic

A; Reference number: A28079; MUID:88228050; PMID:3372523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 361-911 <HAM>
C;Comment: Band 3 is the major integral glycoprotein of the erythrocyte membrane. A dime
A;Title: Amino acid sequence of the N(alpha)-terminal 201 residues of human erythrocyte A;Reference number: A92430; MUID:83238395; PMID:6345535 A;Accession: A93430 A;Accession: A93430 A;Accession: A;A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biochem. 122, 577-585, 1997
A.Title: Proteolytic cleavage sites of band 3 protein in alkali-treated membranes: Fidel
A.Reference number: PC4403; MUID:98006310; PMID:9348087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 1-201;220-292;307-308,'R',310-312,'S',314-329,'K',331-333;347-370 < YAN1>
A; Residues: 1-201;220-292;307-308,'R',310-312,'S',314-329,'K',331-333;347-370 < YAN1>
B; Cobb, C. E.; Beth, A. H.
Biochemistry 29, 8288-8290, 1990
A; Title: Identification of the eosinyl-5-maleimide reaction site on the human erythrocyt
A; Reference number: A35835; MUID:91070049; PMID:1701324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tryptic digestion. Confo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <OKU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Realdues: 834-842, "x, 844-911 <KAW>
A;Realdues: 834-842, "x, 844-911 <KAW>
A;Realdues: 834-862, "x, 844-911 <KAW>
A;Realdues: By-851 was shown to bind the affinity label pyridoxal phosphate, a substrate f
B;Yannoukakos, D.; Vasseur, C.; Blouquit, Y.; Bursaux, E.; Wajcman, H.
Biochim: Biochimys, Acter 998, 43-49, 1989
A;Title: Primary structure of the cytoplasmic domain of human erythrocyte protein band
A;Title: Primary Structure of the cytoplasmic domain of human erythrocyte protein band
A;Reference number: S05523; MUID:90001294; PMID:2790053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 361-364, X', 366-372:424-429, X', 431-434 <COB>
A; Residues: 361-364, X', 366-372:424-429, X', 431-434 <COB>
A; Rote: Lys-430 is labeled by eosiny1-5-maleimide (EMA) in intact erythrocytes
R; Yannoukakos, D.; Vasseur, C.; Driancourt, C.; Blouquit, Y.; Delaunay, J.; Wajcman, Blood 78, 1117-1120, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A; Readidues: 1-55, Er, 57-69 < YANZ>
A; Readidues: 1-55, Er, 57-69
A; Note: sequence extracted from NCBI backbone (NCBIP:49829)
A; Note: sequence of a common polymorphic form designated band 3 Memphis B; Kang, D; Okubo, K.; Hamasaki, N; Kuroda, N.; Shiraki, H.
J. Biol. Chem. 267, 19211-19217, 1992
A; Title: A structural study of the membrane domain of band 3 by tryptic A; Reference number: A44116; MUID:92406862; PMID:1527044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 427-436;479-519;538-540;559-566;809-817;825-841;849-857
A;Note: Lys-539 and Lys-851 were shown to bind the same molecule of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Hamasaki, N.; Okubo, K.; Kuma, H.; Kang, D.; Yae, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A44116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: A28079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PC4403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S05523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: A35835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Status:
```

Gaps

ö

; 0

5e-08;

<TM04> <TM06> <TM09> <TM10> <TM11>

<TM08>

<TM14>

ö

Gaps

ó

Length 848; Indels us-10-087-464-2.rpr

 $\boldsymbol{\varsigma}$

```
C; Accession: A31789
R; Alper, S.L.; Kopito, R.R.; Libresco, S.M.; Lodish, H.F.
Biol. Chem. 263, 17092-17099, 1988
A; Title: Cloning and characterization of a murine band 3-related cDNA from kidney and A; Reference number: A31789; MUID:89034212; PMID:3182834
                                                                                                                                                                                                                                                                                  A; Molecule type: mRNÅ
A; Residues: 1-1214 <RUUD>
A; Cross-references: GB:J05166; NID:9203090; PIDN:AAA40799.1; PID:9203091
A; Lindsey, A.E.; Schneider, K.; Simmons, D.M.; Baron, R.; Lee, B.S.; Kopito, R.R.
Proc. Natl. Acad. SCI. U.S.A. 87, S278-5282, 1990
A; Title: Functional expression and subcellular localization of an anion exchanger.clo
A; Reference number: A35770; MUID:90319095; PMID:2371270
                                                                                                                                                              two proteins that are rela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-205, A, 207-924, PG', 927-1017, IV', 1020-1155, ID', 1158-1234 <LIN>
C; Superfamily: band 3 anion transport protein
C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               band 3-related protein, ileum - rabbit
C;Species: Orycholagus cuniculus (domestic rabbit)
C;Species: Orycholagus cuniculus (domestic rabbit)
C;Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 20-Aug-1999
C;Accession: A56764
R;Chow, A.; Dobbins, J.W.; Aronson, P.S.; Igarashi, P.
Am. J. Physiol. 263, 6345-6352, 1992
A;Title: CDNA cloning and localization of a band 3-related protein from ileum.
A;Reference number: A56764; MUID:93035730; PMID:1415547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  band 3-related protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 20-Aug-1999
         C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 20-Aug-1999
C;Accession: A34911; A35770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Accession: A56764
A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-1237 <CHO>
A,Cross-references: GB:S45791; NID:9256659; PIDN:AAB23488.1; PID:9256660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-1237 <ALP>
A;Cross-references: GB:404036; NID:9192132; PIDN:AAA65505.1; PID:9309114
C;Superfamily: band 3 anion transport protein
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                              for
                                                                                             R; Kudrycki, K.E.; Newman, P.R.; Shull, G.E.
J. Biol. Chem. 265, 462-471, 1990
A; Title: CDMA cloning and tissue distribution of mRNAs:
A; Reference number: A34911; MUID:90094439; PMID:2294114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.5%; Score 73; DB 2; Le
83.3%; Pred. No. 0.00099;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.5%; Score 73; DB 2; I
83.3%; Pred. No. 0.00099;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SVTHANALTVMGKASTPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 83,3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
                                                                                                                                                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: A35770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A31789
                                                                                                                                                                                                                           A; Accession: A34911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
C.Daccession: A25104
E.Demuth, D.R.: Showe, L.C.; Ballantine, M.; Palumbo, A.; Fraser, P.J.; Cioe, L.; Rovera EMBO J. 5, 1205-1214, 1986
A;Title: Cloning and structural characterization of a human non-erythroid band 3-like pr A;Reference number: A91039; MUID:86274622; PMID:3015590
A;Accession: A25104
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: 149524
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Cross-references: GB:J02756; NID:g192136; PIDN:AAA37278.1; PID:g553874
A; Cross-references: GB:J02756; NID:g192136; PIDN:AAA37278.1; PID:g553874
B; Demuth, D.R.; Showe, L.C.; Ballantine, M.; Palumbo, A.; Fraser, P.J.; Cloe, L.; Rovers
BMBO J. 5, 1205-1214, 1986
A; Title: Cloning and structural characterization of a human non-erythroid band 3-like pr
A; Reference number: A91039; MUID:86274622; PMID:3015590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Introns: 5/3; 46/1; 70/3; 131/1; 176/2; 217/3; 245/1; 305/3; 376/1; 447/1; 496/3; 561/
C; Superfamily: band 3 anion transport protein
C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M29379; NID:g191741; PIDN:AAA37187.1; PID:g191742 R;Ropito, R.R.; Andersson, M.; Lodish, H.F. B. Biol. Chem. 262, 8032-8040, 1987 A; Biol. Chem. 262, 8032-8040, 1987 A;Title: Structure and organization of the murine band 3 gene. A;Reference number: 149524; MUID:87250387; PMID:3036795
                                                                                                                       A)Cross-references: GB:X02677; NID:g49897; PIDN:CAA26506.1; PID:g49898 R;Kopito, R.R.; Lodish, H.F.
J. Cell. Biochem. 29, 1-17, 1985
A;Title: Structure of the murine anion exchange protein.
A;Reference number: A26086; MUID:86034211; PMID:3840489
A;Accession: A26086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A;Residues: 11-466,'S',468-929 <DEM>
A;Cross-references: GB:X03917; NID:953042; PIDN:CAA27555.1; PID:953043
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:X03918; NID:q33120; PIDN:CAA27556.1; PID:g32121
C;Superfamily: band 3 anion transport protein
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92.9%; Score 91; DB 2; Length 929; 95.0%; Pred. No. 7.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Leuy
. 0.00068;
___3;
A;Reference number: A25314; MUID:85268011; PMID:2410791
A;Accession: A25314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A25104
band 3 protein, nonerythroid (MEB3) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 73; DB;
Pred. No. 0.000
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    749 SVTHANALTVMGKASGPGAA 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SVTHANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 74.5%;
Best Local Similarity 83.3%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SVTHANALTVMGKASTPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    685 SVTHANALTVMSKAVAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A34911
band 3-related protein 2 - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 19; Conserv
                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-929 <KO2>
                                                             A; Molecule type: mRNA
A; Residues: 1-929 <KOP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

ó

ö

us-10-087-464-2.rpr

```
Mol. Cell. Biol. 8, 4416-4424, 1988
A;Title: Two different mRNAs are transcribed from a single genomic locus encoding the A;Reference number: A30816; MUID:89039870; PMID:3185555
A;Accession: A30816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rifievet, B.; Gabillat, N.; Borgese, F.; Motais, R.
EMBO J. 14, 5158-5169, 1995
A;Title: Expression of band 3 anion exchanger induces chloride current and taurine tr
A;Feference number: 559861; MUID:96080151; PMID:7489705
A;Accession: S59861
A;Accession: Speciminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Species: Oncorhynchus mykiss (rainbow trout)
C; Species: Oncorhynchus mykiss (rainbow trout)
C; Date: 07-Apr-1994 #text_change 20-Aug-1999
C; Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 20-Aug-1999
C; Accession: S24318; S36083; S22173
R; Huebner, S.; Michel, F.; Rudloff, V.; Appelhans, H.
Biochen, J. 2865, 17-23, 1992
Biochen J. 2865, 17-23, 1992
A; Title: Amino acid sequence of band-3 protein from rainbow trout erythrocytes derive
A; Reference number: S24318; MUID:92344566; PMID:1637296
                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:Z50848; NID:g1004316; PIDN:CAA90701.1; PID:g1004317
C;Superfamily: band 3 anion transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 15-Feb_1996 #sequence_revision 01-Mar-1996 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-304,'G',306-918 <APP>
A;Cross-references: EMBL:X61699; NID:g64308; PIDN:CAA43868.1; PID:g64309
C;Superfamily: band 3 anion transport protein
C;Keywords: erythrocyte; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 918;
                                                                                                                                                                                                                                                                                                                                           Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 912;
                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              band 3 anion transport protein isoform b - rainbow trout
                                                                                                                                                                                                                                                                                                            Score 71; DB 2; Len
Pred. No. 0.0016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 63; DB 2;
Pred. No. 0.033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
                                                                                                                                                                                                                                                                                                                                                                                                            5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, August 1991
A; Reference number: $22173
A; Accession: $22173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  band 3 anion transport protein - rainbow trout
                                                                                                                                                                                                    A; Cross-references: GB: M23404
C; Superfamily: band 3 anion transport protein
C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.3%; Score 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 71-89;94-114;570-588 <HUE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.3%;
76.5%;
                                                                                                                                                                                                                                                                                                                                              72.4%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-918 <HUE1>
A; Cross-references: EMBL:X61699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SVTHANALTVMGKASTP
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
' Local 13; Conserve
                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-922 <KIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-912 <FIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: S24318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S36083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: S59861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Appelhans, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dation transporter - chicken
C; Species: Gallus gallus (chicken)
C; Species: Gallus gallus (chicken)
C; Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Aug-1999
C; Accession: 150159
R; Cox, J.V.; Lazarides, E.
Mol. Cell. Biol. 8, 1327-1335, 1988
A; Title: Alternative primary structures in the transmembrane domain of the chicken eryth A; Reference number: 150159; MuID:88216609; PMID:2835670
A; Reference number: 150159
A; Accession: 150159
A; Accession: 150159
A; Accession: 150159
A; Residues: 1-844 ccox>
A; Cross-references: GB:M19496; NID:g211211; PIDN:AAA48604.1; PID:g211212
C; Superfamily: band 3 anion transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cipecies: Hono sapiens (man)
Cipecies: Hono sapiens (man)
Cipate: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
Cipate: 22-Nov-1993 #sequence_revision 130.
Cipate: 22-Nov-1999
Cipa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A30816
band 3 anion transport protein (clone pBIIIC1) - chicken
band 3 anion transport protein (clone pBIIIC1) - chicken
C;Species: Gallus gallus (chicken)
C;Species: G1-Dec-1989 #sequence_revision 30-Sep-1991 #text_change 16-Feb-1997
C;Accession: A30816
R;Kim, H.R.C.; Yew, N.S.; Ansorge, W.; Voss, H.; Schwager, C.; Vennstroem, B.; Zenke, M.
                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
A:Experimental source: New Zealand White rabbit, ileal epithelial cells A:Note: sequence extracted from NCBI backbone (NCBIN:115180, NCBIP:115181) C;Superfamily: band 3 anion transport protein
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                          Length 1237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 73; DB 2; Length 124
Pred. No. 0.00099;
0; Mismatches 3; Indels
                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                      Score 73; DB 2;
Pred. No. 0.00099;
0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 71; DB 2;
Pred. No. 0.0014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
                                                                                                                                                                                                                                                                                                        1057 SVTHANALTVMSKAVAPG 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1060 SVTHANALTVMSKAVAPG 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SVTHANALTVMGKASTPG 18
                                                                                                                                          74.5%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74.5%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anion exchange protein 2 - human
                                                                                                                                   Query Match 74.5
Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 74.5
Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

ó

Gaps

ó

Indels

5,

Mismatches

Score 61; DB 2; Length 1227; Pred. No. 0.097;

```
Rikopito, R.R.; Lee, B.S.; Simmons, D.M.; Lindsey, A.E.; Morgans, C.W.; Schneider, K. Cell. 59, 927-937. 1989 Astrile: Regulation of intracellular pH by a neuronal homolog of the erythrocyte anio A; Reference number: A33638; MUID:90075236; PMID:2686841
                              C;Species: Mus musculus (house mouse)
C;Date: 02-Feb-1990 #sequence_revision 02-Feb-1990 #text_change 20-Aug-1999
                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1227 <KOP>
A;Cross-references: GB:M28383; NID:g191735; PIDN:AAA37184.1; PID:g309095
C;Superfamily: band 3 anion transport protein
     erythrocyte anion exchanger homolog AE3 - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: September 3, 2003, 11:51:18
Job time : 19.25 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 72.2%;
Matches 13; Conservative
                                                                                  C; Accession: A33638
                                                                                                                                                                                                                    A; Accession: A33638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Note: this translation is not annotated in GenBank entry RATAE3A, release 111.0; this A; Note: sequence extracted from NCBI backbone (NCBIN:96971, NCBIP:96975)
A; Accession: B42497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 20-Aug-1999
C;Accession: B34911
R;Kudrycki, K.E.; Newman, P.R.; Shull, G.E.
R;Kudrycki, K.E.; Newman, P.R.; Shull, G.E.
A;Title: Chem. 265, 462-471, 1990
A;Title: CDNA cloning and tissue distribution of mRNAs for two proteins that are related A;Reference number: A34911; MUID:90094439; PMID:2294114
                                                                                                                                                                                                                                                                                                                                                                                             Rilin, S.C.; Kudrycki, K.E.; Shull, G.E.
J. Blol. Chem. 267, 7927-7935, 1992
A; Hitle: The predicted translation product of a cardiac AE3 mRNA contains an N terminus A; Telte: The predicted translation product of a cardiac AE3 mRNA contains an N terminus A; Reference number: A42497; MUID:92218461; PMID:1560021
A; Accession: A42497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Molecule type: DNA
A;Residues: 1-73, C. CLIN2>
A;Cross-references: GB:M87060; NID:g202770; PIDN:AAA40692.1; PID:g202771
A;Experimental source: tissue type spleen
C;Superfamily: band 3 anion transport protein
C;Keywords: alternative splicing; cardiac muscle; heart; transmembrane protein
                                                                                                                                                                                                                                                                                                                  C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 07-Dec-1999
C;Accession: A42497; B42497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Status: preliminary
A:Molecule type: mRNA
A:Molecule type: mRNA
A:Residues: 1-127 < KUDA:
A:Cross-references: GB:J05167; NID:g203088; PIDN:AAA40798.1; PID:g203089
C:Superfamily: band 3 anion transport protein
C:Keywords: transmembrane protein
                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 61; DB 2; Length 1030;
Pred. No. 0.081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Indels
                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Indels
                                                                                                                                                                                                                                                                anion exchanger 3, cardiac splice form - rat N; Alternate names: AE3; chloride/bicarbonate exchanger 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 61; DB 2;
Pred. No. 0.097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-1030 <LINI>A;Cross-references: GB:M87060; NID:g202770
  Pred. No. 0.033;
                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVTHVNALTVMRTAIAPG 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVTHVNALTVMRTAIAPG 868
                        ö
                                                                                                           1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.2%;
72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.28;
72.28;
  76.5%;
                                                                             1 SVTHANALTVMGKASTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 72.28
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   band 3-related protein 3 - rat
Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: B34911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B34911
                                                                                ò
                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

RESULT 15 A33638

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

3, 2003, 11:41:03; Search time 17.25 Seconds (without alignments) 111.500 Million cell updates/sec September Run on:

US-10-087-464-3 96 1 GKASTPGAAAQIQEVKEQRI 20 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		٠																												
	Description	band 3 anion trans	band 3 anion trans	band 3 protein - m	anion transporter	c	band 3 protein, no	3-	band 3-related pro	band 3-related pro	n exchange	band 3 anion trans	anion exchanger 3,	band 3-related pro	erythrocyte anion	anion exchanger 3	apoptosis associat	ABC transporter, A	sugar-phosphate de	sugar-phosphate de	polymerase-associa	polymerase-associa	hypothetical prote	hypothetical prote	nucleobindin precu		hypothetical prote		o.	
SUMMARIES																														
SUM	а	взни	A33810	A25314	I50159	A30816	A25104	A34911	A31789	A56764	S21086	S31828	A42497	B34911	A33638	I38496	T03748	F75377	D82644	E82644	RRNZYA	RRNZED	T28858	T36321	JC1224	155472	D86178	T48429	F95386	D90938
	DB	7	7	7	7	7	7	ď	7	~	7	7	7	~	7	~	N	~	7	7	Н	_	7	7	~	7	7	7	7	7
	Query Match Length	911	848	929	844	922	865	1234	1237	1237	1240	357	1030	1227	1227	1232	1317	346	362	329	391	391	826	391	455	459	1369	1495	324	416
ф	Query	100.0	92.7	92.7	63.5	63.5	60.4	60.4	60.4	60.4	60.4	56.2	56.2	56.2	56.2	56.2	52.1	50.0	50.0	46.9	46.9	46.9	46.9	45.8	45.8	45.8	45.8	45.8	44.8	44.8
	Score	96	68	89	61	61	28	28	28	28	28	54	54	5.4	54	54	20	48	48	45	45	45	45	44	44	44	44	44	43	43
	Result No.	1	7	æ	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	. 21	22	23	24	25	56	27	28	59

probable transport	hypothetical metab	coronin-like prote	non-histone chromo	D-alanyl-D-alanine	hypothetical prote	probable myosin he	probable sodium bi	hypothetical prote	. hypothetical prote	collagen - nematod	acidic calmodulin-	flagellar biosynth	flagellar biosynth	probable dimethyla	protein F5M15.22 [
н85786	A64937	T38258	T38936	C97305	S60961	A71441	T37460	T22491	C84482	B44984	A46597	AI2647	Н97429	H95942	B86338
(3	7	~	~	~	~	~	7	~	~	~	~	~	7	~	7
416	452	601	108	241	448	527	1119	1175	159	210	220	251	251	264	265
44.8	44.8	44.8	43.8	43.8	43.8	43.8	43.8	43.8	42.7	42.7	42.7	42.7	42.7	42.7	42.7
43	43	43	42	42	42	42	42	42	41	41	41	41	41	41	41
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 B3HU Mand 3 anion transport protein, erythrocyte - human N;Alternate names: carrier family 4, anion exchanger, member 1; erythroid anion exchan C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: 33-Aug-1984 #sequence_revision 03-Oct-1995 #text_change 22-Jun-1999 C;Accession: A36218; S03074; I39408; I39409; A92237; A26507; A92430; A90323; A28079; R;Lux, S.E.; John, K.M.; Kopito, R.R.; Lodish, H.F.
R;Lux, S.E.; John, K.M.; Kopito, R.R.; Lodish, H.F.
C; Accession: A36218; S03074; I39408; I39409; A92237; A26507; A92430; A90323; A28079;
C;Date: 03-Aug-1984 #sequence_revision 03-Oct-1995 #text_change 22-Jun-1999
C;Species: Homo sapiens (man)
N; Alternate names: carrier family 4, anion exchanger, member 1; erythroid anion excha
band 3 anion transport protein, erythrocyte - human
ВЗНО
RESULT 1

Vitile: Cloning and characterization of band 3, the human erythrocyte anion-exchange A; Reference number: A36218; MUD:90083213; PMID:2594752
A; Accession: A36218
A; Residues: 1-911 < LUX>
A; Molecule type: mRNA
A; Residues: 1-911 < LUX>
A; Reference number: S03074; MUD:89134172; PMID:3223947
A; Reference number: S03074; MUID:89134172; PMID:3223947
A; Residues: 1-55, E', 57-911 < TAN>
A; Residues: 1-55, E', 57-911 < TAN>
A; Residues: 1-55, E', 57-911 < TAN>
A; Residues: 1-56, E', 57-911 < TAN>
A; Reference number: 139408; MUD:88031311; PMID:3478298
A; Residues: 37-56 < CSHO1>
A; Accession: 139409
A; Accession: 13940

A; Residues: 118-161 (SHO2>
A; Residues: 118-161 (SHO2>
A; Residues: 118-161 (SHO2>
A; Cross-references: GB:M16979; NID:g178218; PIDN:AAA51671.1; PID:g553169
A; Title: Orientation of the band 3 polypeptide from human erythrocyte membranes. Iden
A; Accession: A92237
A; Molecule type: protein
A; Residues: 1-3 ADRI>
A; Molecule type: protein
A; Residues: 1-3 ADRI>
Biochem. J. 205, 465-475, 1982
A; Title: Characterization and partial sequence of di-iodosulphophenyl isothiocyanate-A; Reference number: A26507; MUID:83074521; PMID:7150226
A; Molecule type: protein
A; Recession: A26507
A; Molecule type: protein
A; Residues: 437-473; 360-364, 'D', '366-369 < MAW>
B; Kaul, R. K.; Murthy, S.N.P.; Reddy, A.G.; Steck, T.L.; Kohler, H.
B; Biol. Chem. 258, 7981-7990, 1983

ø

predicted predicted

us-10-087-464-3.rpr

ო

Sep

Wed

```
C; Keywords: acetylated amino end; glycoprotein; ion transport; phosphoprotein; transm
        C;Comment: Band 3 has at least two functional domains. Its integral domain mediates ing sites for cytoskeletal proteins, glycolytic enzymes, and hemoglobin.
                                                                                                                                                                                                                                                                                                                                                             Toomain: transmembrane #status predicted <TW04>

Toomain: transmembrane #status predicted <TW04>

Toomain: transmembrane #status predicted <TW05>

Toomain: transmembrane #status predicted <TW06>

Toomain: transmembrane #status predicted <TW06>

Toomain: transmembrane #status predicted <TW09>

Toomain: transmembrane #status predicted <TW09>

Toomain: transmembrane #status predicted <TW10>

Toomain: transmembrane #status predicted <TW10>

Toomain: transmembrane #status predicted <TW12>

Toomain: transmembrane #status predicted <TW12>

Toomain: transmembrane #status predicted <TW13>

Toomain: transmembrane #status predicted <TW14>

Toomain: transmembrane #status predicted <TW14>

Toomain: transmembrane #status predicted <TW14>

Toomain: transmembrane #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          site: anion (Lys) #status experimenta
                                                                                                                                               A;Map position: 17q21-17q22
C;Superfamily: band 3 anion transport protein
                                                                                                                                                                                                                                  F;1-403/Region: cytoskeletal protein binding
                                                                                                                  GDB:119874; OMIM:109270
                                                                                                                                                                                                                                                                                           transmembrane #status
                                                                                                                                                                                                                                                                                                                        transmembrane #status
                                                                                                                                                                                                                                                                                                                                                  transmembrane #status
                                                                                                                                                                                                                                                                    anion antiporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               band 3 anion transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-848 <KUD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    590,851/Binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                     A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 642/Binding site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: A33810
                                                                                                                                                                                                                                                         F; 404-911/Region:
                                                                                                                                                                                                                                                                                         F;405-427/Domain:
                                                                                                                                                                                                                                                                                                                  F;435-457/Domain:
                                                                                                                                                                                                                                                                                                                                                  F;459-479/Domain:
                                                                                                                                                                                                                                                                                                                                                                            ;491-507/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                            F;568-588/Domain:
F;604-624/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;659-680/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;861-881/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;701-721/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;723-743/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64-780/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;764-780/Domain:
F;785-806/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A25314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Abstraction of the same H-2DIDS (ARA)

**Reference number: A49717; MUID:94124538; PMID:8294441

**Reference number: A49717; MUID:94124538; PMID:8294441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: PC4403
A;Molecule type: protein
A;Residues: 361-911 <HAM>
C;Comment: Band 3 is the major integral glycoprotein of the erythrocyte membrane. A dime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A. Molecule type: protein

A. Residues: 1-55, E',57-69 <TAN2>

A. Note: sequence extracted from NCBI backbone (NCBIP:49829)

A. Note: sequence of a common polymorphic form designated band 3 Memphis

B. Kang, D.; Okubo, K.; Hamasaki, N.; Kuroda, N.; Shiraki, H.

J. Biol. Chem. 267, 19211-19217, 1992

A. Title: A structural study of the membrane domain of band 3 by tryptic digestion. Confc

A. Reference number: A44116; MUID:92406862; PMID:1527044
                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A; Moses: 559-670 < ARNO
A; Notes: Lys-590 was shown to bind phenyl isothiocyanate, an inhibitor of anion transport
B; Kawano, Y.; Okubo, K.; Tokunaga, F.; Miyata, T.; Iwanaga, S.; Hamasaki, N.
B; Blol. Chem. 263, 8322-8328, 1988
A; Title: Localization of the pyridoxal phosphate binding site at the COOH-terminal regic
A; Reference number: A28079; MUID:88228050; PMID:3372523
the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Wolecule type: protein
A;Residues: 361-372;390-399;604-613;632-639;647-656;699-729;731-743;761-781;818-826 <KAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Molecule type: protein
A; Residues: 427-436; 479-519; 538-540; 559-566; 809-817; 825-841; 849-857 < OKU>
A; Note: Lys-539 and Lys-851 were shown to bind the same molecule of the anion transport R; Hamasaki, N.; Okubo, K.; Kuma, H.; Kang, D.; Yae, Y.
A; Blochem. 122, 577-885, 1997
A; Title: Proteolytic cleavage sites of band 3 protein in alkali-treated membranes: Fidel A; Reference number: PC4403; MUID:98006310; PMID:9348087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blood 78, 1117-1120, 1991
A;Title: Human erythrocyte band 3 polymorphism (band 3 Memphis): characterization of
A;Reference number: A44933; MUID:91329825; PMID:1678289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: A44933
```

```
band 3 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 20-Aug-1999
C;Accession: A25314; A26086; I49524; B25104
R;Kopito, R.R.; Lodish, H.F.
Nature 316, 234-238, 1985
A;Title: Primary structure and transmembrane orientation of the murine anion exchange
                                                                                                                                                                                                                                                                                                                                                                                                           C,Accession: A33810
R;Kudrycki, K.E.; Shull, G.E.
J. Biol. Chem. 264, 8185-8192, 1989
A;Title: Primary structure of the rat kidney band 3 anion exchange protein deduced fr
A;Reference number: A33810; MUID:89255254; PMID:2722777
                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                          C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 20-Aug-1999
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:J04793; NID:q203092; PIDN:AAA40800.1; PID:q203093
                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
Score 96; DB 1; Len
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: band 3 anion transport protein C;Keywords: alternative splicing; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 92.7%; Score 89; DB 2; Le Local Similarity 95.0%; Pred. No. 1.2e-05; les 19; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             742 GKASTPGAAAQIQEVKEQRI 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GKASTPGAAQIQEVKEQRI 20
                                                                                                  .
0
                                                                                                                                                     1 GKASTPGAAAQIQEVKEQRI
                                                                    ilarity 100.0%;
Conservative (
```

```
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Accession: A30816
A;Title: Two different mRNAs are transcribed from a single genomic locus encoding the A;Reference number: A30816; MuID:89039870; PMID:3185555
A;Accession: A30816
A;Accession: A30816
A;Accession: A30816
A;Accession: A30816
A;Accession: A30816
C;Superferences: GB:M23404
C;Superfamily: band 3 anion transport protein
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Species: Homo sapiens (man)
C; Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
C; Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
C; Accession: A25104
R; Demuth, D. R.; Showe, L.C.; Ballantine, M.; Palumbo, A.; Fraser, P.J.; Cioe, L.; Rov EMBO J. 5, 1205-1214, 1986
A; Title: Cloning and structural characterization of a human non-erythroid band 3-like A; Title: Cloning and structural characterization of a human non-erythroid band 3-like A; Reference number: A91039; MUID:86274622; PMID:3015590
A; Accession: A25104
A; Molecule type: mRNA
A; Residues: 1-865 <DEN>
A; Cross-references: GENXO3918; NID:932120; PIDN:CAA27556.1; PID:932121
C; Superfamily: band 3 anion transport protein
C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        band 3-related protein 2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 20-Aug-1999
C;Accession: A34911; A35770
R;Kudrycki, K.E.; Newman, P.R.; Shull, G.E.
J. Biol. Chem. 265, 462-471, 1990
A;Title: cDNA cloning and tissue distribution of mRNAs for two proteins that are rela
A;Reference number: A34911; MUID:90094439; PMID:2294114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: A34911
A; Status: preliminary
A; Molecule type: mRM
A; Molecule type: mRM
A; Residues: 1-1234 cKUD>
A; Cross-references: GB:J05166; NID:g203090; PIDN:AAA40799.1; PID:g203091
A; Cross-references: GB:J05166; NID:g203090; PIDN:AAA40799.1; PID:g203091
B; Linddsey, A.E.; Schneider, K.; Simmons, D.M.; Baron, R.; Lee, B.S.; Kopito, R.R.
Proc. Natl. Acad. Sci. U.S.A. 87, 5278-5282, 1990
A; Title: Functional expression and subcellular localization of an anion exchanger clo
A; Reference number: A35770; MUID:90319095; PMID:2371270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.5%; Score 61; DB 2; Length 922; 60.0%; Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A25104
band 3 protein, nonerythroid (MEB3) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
0.73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 58; DB 2
Pred. No. 0.73;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GKASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 KASTPGAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 60.4%;
Best Local Similarity 63.2%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 60.0 nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA,
A; Residues: 4-70', Xr, 799-902 (RES>
A; Residues: 4-70', Xr, 799-902 (RES>
A; Residues: 4-70', Xr, 799-902 (RES>
A; Cross-references: GB:J03756; NID:9192136; PIDN:AAA37278.1; PID:9553874
B; Demuth, D.R.; Showe, L.C.; Ballantine, M.; Palumbo, A.; Fraser, P.J.; Cloe, L.; Rovera
Brbo J. 5, 1205-1214, 1986
A; Title: Cloning and structural characterization of a human non-erythroid band 3-like pr
A; Reference number: A91039; MUID:86274622; PMID:3015590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Aug-1999
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Aug-1999
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Aug-1999
C;Date: 13-Sep-1996 #sequence_revision 150.189
Mol. Cell. Biol. 8, 1327-1335, 1988
A;Title: Alternative primary structures in the transmembrane domain of the chicken eryth A;Reference number: 150159; MUID: 88216609; PMID: 2835670
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Genetics:
A; 46/1; 70/3; 131/1; 176/2; 217/3; 245/1; 305/3; 376/1; 447/1; 496/3; 561/
C;Superfamily: band 3 anion transport protein
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-929 <KO2>
A; Residues: 1-929 <KO2>
A; Cross-references: GB:M29379; NID:g191741; PIDN:AAA37187.1; PID:g191742
A; Cross-references: GB:M29379; NID:g191741; PIDN:AAA37187.1; PID:g191742
B; Kopito. R. R.; Andersson, M.; Lodish, H.F.
J. Biol. Chem. 262, 8035-8040, 1987
A; Title: Structure and organization of the murine band 3 gene.
A; Reference number: 149524; MUID:87250387; PMID:3036795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-844 <COX>
A;Cross-references: GB:M19496; NID:g211211; PIDN:AAA48604.1; PID:g211212
C;Superfamily: band 3 anion transport protein
                                                                       A; Molecule type: mRNA
A; Readidues: 1-929 < ROPD
A; Readidues: 1-920 < ROPD
A; Cross-references: GBPD
A; Cross-references: GBPD
B; Kopito, R.R.; Lodish, H.F.
J. Cell. Biochem. 29, 1-17, 1985
A; Title: Structure of the murine anion exchange protein.
A; Reference number: A26086; MUID:86034211; PMID:3840489
A; Accession: A26086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 11-466,'S',468-929 <DEM>
A; Cross-references: GB:X03917; NID:g53042; PIDN:CAA27555.1; PID:g53043
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 89; DB 2; Length 929;
Pred. No. 1.3e-05;
); Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
          A; Reference number: A25314; MUID:85268011; PMID:2410791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 61; DB 2
Pred. No. 0.25;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GKASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GKASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 92.7%;
Local Similarity 95.0%;
hes 19; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 63.5%;
Best Local Similarity 60.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anion transporter - chicken
                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: I49524
```

Query Match

Best Loc Matches

ŏ qq A;Accession: A35770
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual A;Molecule type: mRMA
A;Molecule type: mRMA
A;Residues: 1-205,'A',207-924,'PG',927-1017,'IV',1020-1155,'ID',1158-1234 <LIN>
C;Superfamily: band 3 anion transport protein

A30816 band 3 anion transport protein (clone pBIIIC1) - chicken

||::||| | |||||||: GKSAVPGERAHIVEVKEQRL 694

675

ŏ q RESULT 5

```
A; Residues: 1-1030 KLINI>
A; Cross-references: GB:M87060; NID:g202770
A; Note: this translation is not annotated in GenBank entry RATAE3A, release 111.0; th
A; Note: sequence extracted from NCBI backbone (NCBIN:96971, NCBIP:96975)
A; Accession: B42497
  A;Title: Complete nucleotide sequence of band 3 related anion transport protein AE2 A;Reference number: S21086; MUID:92223115; PMID:1562608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 29-Oct-1999 #seguence_revision 29-Oct-1999 #text_change 07-Dec-1999
C;Accession: A42497; B42497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rilin, S.C.; Kudrycki, K.E.; Shull, G.E.
J. Biol. Chem. 267, 7927-7935, 1992
A; Title: The predicted translation product of a cardiac AE3 mRNA contains
gene, and identification of an alternative transcription initiation site.
A; Reference number: A42497; WUID:92218461; PMID:1560021
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X70797; NID:g28427; PIDN:CAA50067.1; PID:g939883 C;Superfamily: band 3 anion transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-73. 'E' <LIN2>
A; Cross-references: GB M87060; NID: 9202770; PIDN: AAA40692.1; PID: 9202771
A; Experimental source: tissue type spleen
C; Superfamily: band 3 anion transport protein
C; Superfamily: band 3 anion transport protein
C; Keywords: alternative splicing; cardiac muscle; transmembrane pu
                                                                                                                                                   PIDN:CAA44067.1; PID:928425
                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                   Length 1240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 357;
                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anion exchanger 3, cardiac splice form - rat
N;Alternate names: AE3; chloride/bicarbonate exchanger 3
C;Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5,
                                                                                                                                                                                                                                                      5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              band 3 anion transport protein - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Gehrig, H.; Appelhans, H. submitted to the EMBL Data Library, January 1993 A;Reference number: S31828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 54; DB;
Pred. No. 1.3;
2; Mismatches
                                                                                                                                                                                                                                                      DB
                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                              A;Cross-references: EMBL:X62137; NID:928424; EC;Superfamily: band 3 anion transport protein C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                   58;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N; Alternate names: anion exchange protein 3
                                                                                                                                                                                                                                                        Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                  1072 KAVAPGDKPKIQEVKEQRV 1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                     2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.2%;
                                                                                                                                                                                                                                                      60.4%;
illarity 63.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 ASTPGAAAQIQEVKEORI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C,Species: Homo sapiens (man)
C,Date: 06-Jan-1995 #sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                               A; Residues: 1-1240 <GEH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-357 <GEH>
                                                 A; Accession: S21086
A; Status: preliminary
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S31828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: S31828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                      δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                        A31789

Band 3-related protein - mouse

Band 3-related protein - mouse

C.Species: Mus musculus (house mouse)

C.Species: Mus musculus (house mouse)

C.Species: Mus musculus (house mouse)

C.Species: A31789

C.Accession: A31789

C.Accession: A31789

A.Title: Cloning and characterization of a murine band 3-related cDNA from kidney and france number: A31789

A.Title: Cloning and characterization of a murine band 3-related cDNA from kidney and francession: A31789

A.Title: Cloning and characterization of a murine band 3-related cDNA from kidney and francession: A31789

A.Reference number: A31789

A.Residues: 1-1237 AALP

A.Residues: 1-1237 AALP

A.Coss.references: GB.JO4036; NID:9192132; PIDN:AAA65505.1; PID:9309114

C.Superfamily: band 3 anion transport protein

C.Reywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Asorte: Observed protein, ileum - rabbit
band 3-related protein, ileum - rabbit
C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Date: OB-Sep-1995 #sequence_revision OB-Sep-1995 #text_change 20-Aug-1999
C; Accession: A56764
R; Chow, A.; Dobbins, J.W.; Aronson, P.S.; Igarashi, P.
Am. J. Physiol. 263, G345-G352, 1992
A; Title: CDNA cloning and localization of a band 3-related protein from ileum.
A; Accession: A56764
A; Accession: A56764
A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; CTOSS-references: GB:S45791; NID:G256659; PIDN:AAB23488.1; PID:g256660
A; CTOSS-references: GB:S45791; NID:G256659; DIDN:AAB23488.1; PID:g256660
A; Experimental source: New Zealand White rabbit, ileal epithelial cells
A; Note: sequence extracted from NCBI backbone (NCBIN:115180, NCBIP:115181)
C; Superfamily: band 3 anion transport protein
                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anion exchange protein 2 - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C;Accession: S21086
C;Ricellin, H.; Mueller, W.; Appelhans, H.
Biochim, Biophys. Acta 1130, 326-328, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                 Length 1234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1237;
                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5;
                                                                                               5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.4%; Score 58; DB 2; ilarity 63.2%; Pred. No. 1; Conservative 2; Mismatches
                                                   2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 58; DB 2;
Pred. No. 1;
                                                 Score 58; DB 2
Pred. No. 1;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ed. No. 1;
Mismatches
                                                                                                                                                                             1069 KAVAPGDKPKIQEVKEQRV 1087
                                                                                                                                                 2 KASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KASTPGAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KASTPGAAAQIQEVKEQRI 20
                                                 Query Match 60.4%;
Best Local Similarity 63.2%;
Matches 12; Conservative
C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.4%;
ilarity 63.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mu.
Local Sim.
12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
```

ö

N termin

an

0;

Gaps

;

Score 54; DB 2; Length 1232; Pred. No. 4.2; 2; Mismatches 5; Indels

20

```
A, Residues: 1-1232 <RES>
A, Cross-references: EMBL:U05596; NID:g476221; PIDN:AAA50748.1; PID:g476222
C, Superfamily: band 3 anion transport protein
                                                                                                                                                                                                                                                                                                                                   Search completed: September 3, 2003, 11:51:19 Job time: 18.25 secs
                                                                                                                                                                                                                                       3 ASTPGAAAQIQEVKEQRI
                                                                                                                  Query Match
Best Local Similarity 61.1%;
Matches 11; Conservative
  A; Molecule type: mRNA
                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                 R; Kudrycki, K.E.; Newman, P.R.; Shull, G.E.
7. Biol. Chem. 265, 462-471, 1990
A;Title: CDNA cloning and tissue distribution of mRNAs for two proteins that are related
A;Reference number: A34911; MUID:90094439; PMID:2294114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Molecular cloning, expression, and chromosomal localization of two isoforms of A;Reference number: 138496; MUID:95008042; PMID:7923606
A;Accession: 138496
A;Status: preliminary; translated from GB/EWBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Kopito, R.R.; Lee, B.S.; Simmons, D.M.; Lindsey, A.E.; Morgans, C.W.; Schneider, K. Cell 59, 927-937, 1989
A;Title: Regulation of intracellular pH by a neuronal homolog of the erythrocyte anion A;Reference number: A33638; MUID:90075236; PMID:2686841
A;Accession: A33638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Yannoukakos, D.; Stuart-Tilley, A.; Fernandez, H.; Fey, P.; Duyk, G.; Alper, Circ. Res. 75, 603-614, 1994
                                                                                                                                                                                                                                                      C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 20-Aug-1999
C;Accession: B34911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anion exchanger 3 brain isoform - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Mus musculus (house mouse)
C;Date: 02-Feb-1990 #sequence_revision 02-Feb-1990 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
*Residues: 1-1277 <KOPS /
A;Cross-references: GB:MZ8383; NID:g191735; PIDN:AAA37184.1; PID:g309095
C;Superfamily: band 3 anion transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIDN: AAA40798.1; PID: 9203089
                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                        Indels
                        ..
..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 54; DB 2;
Pred. No. 4.2;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
Best Local Similarity 61.1%; Pred. No. 3.5;
Matches 11; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             erythrocyte anion exchanger homolog AE3 - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: GB.J05167; NID:g203088; PIC; Superfamily: band 3 anion transport protein C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 54;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1061 AIAPGDKPQIQEVREQRV 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 ASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 ASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 61.1%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 56.2%;
Best Local Similarity 61.1%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 ASTPGAAAQIQEVKEQRI
                                                                                                                                                                                                                                       3-related protein 3 - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1227 <KUD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: A33638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: 138496
                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: B34911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
                                                                                                                                                                                                                                         band
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                        ò
                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

THIS PAGE BLANK (USPTO)

```
September 3, 2003, 11:40:18 ; Search time 44.5 Seconds (without alignments) 115.979 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                       830525
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                    830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                               OM protein - protein search, using sw model
                                                                                                                                                               US-10-087-464-3
96
1 GKASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_fungi:*
sp_human:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPTREMBL_23:*
L: sp_archea:*
2: sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_plant:*
sp_rodent:*
sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_archeap:*
                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                  Sequence:
                                                                                                Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	1013411011	Q91ze7 rattus norv	Q9tuq0 bos taurus	Q9xsw5 bos taurus	Q90579 qallus qall	035225 cynomys lud	Q991t5 mus musculu	O9tu75 sus scrofa	Q8taq3 homo sapien	Q90710 gallus gall	Q9uey4 homo sapien	Q9uey5 homo sapien	Q99654 homo sapien	homo	Q99416 homo sapien	OMO	4 mus
SUMMARIES	; 10 11 11 11 11 11 11 11 11 11 11 11 11 1	Q91ZE7	Q9TUQ0	O9XSW5	090579	035225	Q99LT5	Q9TU75	Q8TAG3	090710	Q9UEY4	Q9UEY5	099654	Q9UEY6	099416	013717	Q9ERP4
DB		11	9	9	13	11	11	9	4	13	4	4	4	4	4	4	11
% Query Match Length DB		849	855	930	844	103	466	622	1159	1219	1227	1232	1241	1241	357	357	1030
% Query Match		92.7	72.9	72.9	63.5	60.4	60.4	60.4	60.4	60.4	60.4	60.4	60.4	60.4	56.2	56.2	56.2
Score		89	70	70	61	28	28	28	58	58	58	28	58	28	54	54	54
Result No.		Н	7	e	4	S	9	7	80	6	10	11	12	13	14	15	16

0; Gaps

Query Match 92.7%; Score 89; DB 11; Length 849; Best Local Similarity 95.0%; Pred. No. 9.7e-06; Matches 19; Conservative 0; Mismatches 1; Indels

QY Db RESULT 2

Ogerp5 mus musculu P79877 lampetra ja Ogeche2 mus musculu O35211 mus musculu Ogecp63 mus musculu Ogecp63 mus musculu Ogecp63 vylella fas Ogeq6 vylella fas Ogeq7 vylella fas Ogeq8 mumps virus Ogeq7 mumps virus Ogeq7 mumps virus Ogen6 mumps virus		PRT; 849 AA. eated) st sequence update) st annotation update) Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.	SEQUENCE FROM N.A. TISSUE-COLOIN TISSUE-COLOIN TISSUE-COLOIN THE H., Binder H.J., Rajendran V.M.; "Molecular cloning and characterization of band 3 anion exchange brotein (AEI) mRNA from rat colon."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AY030082; AAK88733.1; - InterPro; IPR001717; Anion_exchange. InterPro; IPR001201; HCO3-cotranspt. PFANTYS; PR01231; HCO3-TRNSPORT. TIGRRAMS; TIGR00834, aes; I. PROSITE; PS00129; ANION_EXCHANGER_1; I. PROSITE; PS00220; ANION_EXCHANGER_2; I. SEQUENCE 849 AA; 94312 MM; E4B200780CB07D3A CRC64;
Q9ERP5 P79877 P79877 P79877 Q8CB63 Q9CB63 Q9PC04 Q9C041 Q9C071 Q9DQA3 Q91416 Q90416 Q91416 Q9	ALIGN	u a a ⋅	, Rajendran V.M.; and characterizat. if from rat colon."; i) to the EMBL/Gen; K38733.1; 7; Anion_exchange. 0; HCO3_cotranspt. 3_cotransp; 1. CO3TRNSPORT. 4; ae; 1. ANION_EXCHANGER_1; ANION_EXCHANGER_2; 94312 MW; E4B20
11111111111111111111111111111111111111		19, 19, 23, otei data	indra harat the the '1; '3_cc 3_cc 3_cc 3_cc 3_cc 3_cc
1227 160 160 1317 1317 3346 3364 3394 3391 1253 11253 1183 341 341 341 341 341 341 341 341 341 34		PRELIMINARY; (TrEMBLrel. 19, Le (TrEMBLrel. 23, Le exchange protein. 4) Cus (Rat). etazoa; Chordata; etazoa; Chordata;	E FROM N.A. Colon. Lat cloning and character (AE1) mRNA from rat code (APR-2001) to the E Y030082; AAK38733.1; - PR01231; HCO3_cot in PR01717; Anion_ex of information in PR0131; HCO3_cot information in PR01231; HCO3_Cot in PR01
0 0 0 0 0 0 0 0 0 4 4 4 4 4 4 4 4 4 4 4			FROM N.A. Index H.J. I
6 0 0 0 0 0 4 4 4 4 4 4 4 4 4 4 4 4 4 4	-	1 91ZE7 91ZE7; 91ZE7; 1-DEC- 1	SEQUENCE FROM N.A. TISSUE-COLON. TISSUE-COLON. TISSUE-COLON. Molecular cloning and characterizat protein (AEI) mRNA from rat colon."; Submitted (APR-2001) to the EMBL/Gen EMBL, AY030082; AAK38733.1; InterPro; IPR001717; Anion exchange. InterPro; IPR001717; Anion exchange. InterPro; IPR003020; HCO3_cocranspt. Pran; PR00255; HCO3_cocranspt. PRINTS; PR01231; HCO3TRNSPRT. TIGRRAMS; TIGR00834; ae; 1. PROSITE; PS00219; ANION_EXCHANGER_1; PROSITE; PS00219; ANION_EXCHANGER_2; SEQUENCE 849 AA; 94312 MW; E4B20
11110000000000000000000000000000000000		RESOLT TO 91 LD 12 LD 12 LD 12 LD 12 LD 12 LD 13	

```
NCBI_TaxID=9031;
               Query Match
                                                                                                                                             090579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              035225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
035225
                                                                                                                        RESULT
                                                                                                                                   090579
                                                                                  .
qa
                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Bone marrow;
Koshino I., Inaba M., Matsumoto M., Ono K.;
Koshino I., Inaba M., Matsumoto M., Ono K.;
Koshino I., Inaba M., Matsumoto M., Ono K.;
Fand 3 Bov. Nippon: a nonsense mutation in the band 3 gene associated with decreased mutant mRNA possessing dominant negative effect and dominant hereditary spherocytosis in cattle.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; Ar163826; AAD43593.1;
HSSP; P02730: 1BNX.
InterPro: IPR001717; Anion_exchange.
InterPro: IPR001717; Anion_exchange.
                                                                                                                                                                               TISSUE-Kidney;
Koshino I., Inaba M., Matsumoto M., Ono K.;
"Band 3 Bov. Nippon: a nonsense mutation in the band 3 gene associated with decreased mutant mRNA possessing dominant negative effect and
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                     Score 70; DB 6; Length 855; Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO1231; HCO3TRNSPORT.
TIGRRAMS; TIGR00834; ae; 1.
PROSTITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS0022020; ANION_EXCHANGER_2; 1.
SEQUENCE 930 AA; 104374 MW; 4F6AADFEBAF6A3A1 CRC64;
                                                                                                                                                                                                                             dominant hereditary spherocytosis in cattle.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AF1668928; AAD43354.1; -.
HSSP; P02730; 1BNX.
                                                                                                                                                                                                                                                                         InterPro; IRR001717; Anion_exchange.
InterPro; IRR0010177; Anion_exchange.
InterPro; IRR003020; HCO3_cotranspt.
Prior; PR00955; HCO3_cotranspt.
IGRPAMS; TIGR00834; ae; 1.
TIGRFAMS; TIGR00834; ae; 1.
PROSITE; PS000219; ANION_EXCHANGER_1; 1.
PROSITE; PS000220; ANION_EXCHANGER_2; 1.
SEQUENCE 855 AA; 95643 MW; 06CD037324F69872 CRC64;
                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
             855 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       930 AA.
                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  | ||||| :||| ||||||
686 KDSTPGAVSQIQGVKEQRI 704
                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                     72.9%;
78.9%;
                                   01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAK-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 78.9°
Matches 15; Conservative
             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                            NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9913;
                                                                       Band 3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Band 3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O9XSW5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
O9XSW5
                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Erythroid annion transporter.
Erythroid annion transporter.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transmembrane domain of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cynomys ludovicianus (Black-tailed prairie dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUB-Gall bladder;
Abbedin Z.R., Moser A.J., Roslyn J.J., Abedin M.Z.;
Expression of anion exchange protein 2 (AE-2) in gallbladder epithelia.";
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EmBL; AF012895; AAB66833.1; -
InterPro; IPR003020; HC03_cotranspt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 61; DB 13; Length 844;
  Length 930;
                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfam; PR001531; HCO3_cotransp; 1.
PRINTS; PR01231; HCO3TRNSPORT.
TIGRFAMS; TIGR00834; ae; 1.
TIGRFAMS; TIGR0002020; ANION EXCHANGER_1; 1.
SEQUENCE 844 AA; 93808 MW; C463F993D5974276 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1998 (TrEMBLrel. 05, Created)
1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Anion exchange protein 2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5,
  DB 6;
0.013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 0.35;
                                                                                                                                                                                                                                                                    844 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 AA
                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 0.35
3; Mismatches
  Score 70;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cox J.V., Lazarides E.;
"Alternative primary structures in the chicken erythroid anion transporter.";
MAL. Cell. Biol. 8:1327-1335(1988).
EMBL. M19466; AAA48604.1; -.
HSSP; PO2730; 1BTQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-88216609; PubMed-2835670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 675 GKSAVPGERAHIVEVKEORL 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GKASTPGAAAQIQEVKEQRI 20
                                                                                                                          2 KASTPGAAAQIQEVKEQRI 20
72.9%;
78.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 60.0 Matches 12; Conservative
                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                    PRELIMINARY;
                         Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=45480;
```

```
Zolotarev A.S., Shmukler B.E., Alper S.L.;
"AEZ anion exchanger polypeptide is a homooligomer in pig gastric membranes: a chemical cross-linking study.";
Blochemistry 38 8521-8531(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
similar to solute carrier family 4, anion exchanger, member
(Erythrocyte membrane protein band 3-like 1),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 58; DB 4; Length 1159;
Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
60.4%; Score 58; DB 6; Length 622;
Best Local Similarity 63.2%; Pred. No. 0.77;
Matches 12; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL: BC028601; AARI28601.1; -...
EMBL: BC028601; PARI28601.1; -...
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HC03_cotranspt.
Pfam; PF00955; HC03_cotranspt.
TIGRFAMS; TIGR00834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SEQUENCE 1159 AA; 127747 MW; 9F083A2BEBFF5D74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Brain;
Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER 1 1
SEQUENCE 622 AA; 68713 MW; 58B013462C36E1DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1219 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1159 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                               InterPro; 1PR001717; Anion_exchange.
InterPro; 1PR001717; Anion_exchange.
InterPro; 1PR003020; HCO3_cotranspt.
Pfam; PF001931; HCO3_rotranspr. 1.
PRINTS; PR01231; HCO3TRNSPORT.
TIGREAMS; TIGR00834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seq
01-MRR-2003 (TrEMBLrel. 23, Last anno
AE2-1 anion exchanger.
                                                TISSUE-Stomach;
MEDLINE-99315230; PubMed-10387099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | | | | :|||||||:
991 KAVAPGDKPKIQEVKEQRV 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              || || :||||||||
454 KAVAPGDKPKIQEVKEQRV 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 KASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 60.4%;
Best Local Similarity 63.2%;
Matches 12; Conservative
                                                                                                                                                                                        EMBL; AF120099; AAF00977.1;
HSSP; P02730; 1BTQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          090710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8TAG3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    090710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8TAG3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 090710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8TAG3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E A B B B B B
       ACCOCCOS SELECTION OF THE SELECTION OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           õ
                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-96339307: PubMed-8756692;
Zolotarev A.S., Chernova M.N., Yannoukakos D., Alper S.L.;
"Protoclytic cleavage sites of native AE2 anion exchanger in gastric mucosal membranes.";
Blochemistry 35:10367-10376(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 58; DB 11; Length 466; Pred. No. 0.57;
                                                                                                               Score 58; DB 11; Length 103;
Pred. No. 0.11;
                                                                                                                                                                  5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002234; AAH02234.1; --
MGD; MG1:109351; S16.46.2
InterPro; IPR001717; Anion exchange.
InterPro; IPR001717; Anion exchange.
InterPro; IPR00320; HC03_cotranspt.
PR00955; HC03_cotranspt.
TIGRFAMS; TIGR00834; ae, 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       466 AA; 52003 MW; 481C1108E28D03B1 CRC64;
                                                103 103
103 AA; 11012 MW; 29A99247E768B455 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Chloride-bicarbonate anion exchanger AE2 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                 099LT5;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
11-JUN-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 52.0 kDa protein (Fragment).
SLC4A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               622 AA
                                                                                                                                                                                                                                                                                                                                                                              466 AA
                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 KAVAPGDKPKIQEVKEQRV 316
Pfam; PF00955; HC03_cotransp; 1.
NON_TER 1 103
NON_TER 103 SEQUENCE 103 AA; 11012 MW; 2
                                                                                                                                                                                                              2 KASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                             67 KAVAPGDKPKIQEVKEQRV 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 KASTPGAAAQIQEVKEQRI 20
                                                                                                                      60.4%;
63.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match 60.4%;
Local Similarity 63.2%;
hes 12; Conservative
                                                                                                               Query Match
Best Local Similarity 63.2<sup>3</sup>
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FISSUE-Stomach;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9TU75
Q9TU75;
                                                                                                                                                                                                                                                                                                                                                                              099LT5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                  RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9TU75
                                                                                                                                                                                                                                                                                                                                                          099LTS
       SFFR
                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

ö

Gaps

.; 0

ö

Gaps

; 0

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                      O9UEY5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        099654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLC4A2
                                                                                                                                                                                                                                                                                                                                                      RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                              SOR REPORT OF THE PROPERTY OF 
                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·
AE2.
Gallus gallus (Chicken).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianiae;
                                                                                                                                                                                                                                                                                                                                    COX K. H., Adair Kirk T.L., Cox J.V.;
"Variant AE2 anion exchanger transcripts accumulate in multiple cell
types in the chicken gastric epithelium.";
J. Biol. Chem. 271:8895-8902(1996).
EMBL: U48899; AAC59881.1;
InterPro; IPR001717; Anion_exchange.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR001717; Anion_exchange.
Pfam; PR00155; HCO3_cotranspt.
Pfam; PR00153; HCO3_cotranspt.
TIGRFAMS; TIGR00834; ae; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Vertebrata; Euteleostomi;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-20090621;
Medina J.F., Lecanda J., Acin A., Ciesielczyk P., Prieto J.;
"Tissue-specific N-terminal isoforms from overlapping alternate promoters of the human AEZ anion exchanger gene.";
Blochem. Blophys. Res. Commun. 267:228-235(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=97179202; PubMed=9027488;
Medina J.F., Acin A., Prieto J.;
"Molecular cloning and characterization of the human AE2 anion exchanger (SLC4A2) gene.";
Genomics 39:74-85(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 58; DB 13; Length 1219;
Pred. No. 1.6;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00219; ANION EXCHANGER 1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SEQUENCE 1219 AA; 135288 MW; 25F42A73C3483B21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00219; ANION EXCHANGER 1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SEQUENCE 1227 AA; 135577 MW; 5D47714C17FB8EF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Anion exchanger 2 type b1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1227 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HGO3_cotranspt.
Pfam; PF00955; HGO3_cotransp: 1.
PRINTS; PR01231; HGO37RNSPORT.
                                                                                                                                                                                                                                                                      TISSUE-Proventriculus;
MEDLINE-96224107; PubMed-8621532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1052 KAVAPGDKPKIQEVKEQRV 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U76668; AAF19584.2; JOINED. EMBL; U76668; AAF19584.2; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.48;
63.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGRFAMS; TIGRO0834; ae; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 63.28
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                  NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLC4A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9UEY4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
Q9UEY4
   Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOR RELEASE OF RELEASE OF STREET OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                            Gaps
                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
VCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mediam J.F., Lecanda J., Acin A., Clesielczyk P., Prieto J.;
Missue-specific N-terminal isoforms from overlapping alternate
promoters of the human AE2 anion exchanger gene.";
Biochem. Biophys. Res. Commun. 267:228-235(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=97179202; PubMed=9027488;
Medina J.F., Acin A., Prieto J.;
"Molecular cloning and characterization of the human AE2 anion exchanger (SLC4A2) gene.";
Genomics 39:74-85(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                         ö
    Score 58; DB 4; Length 1227; Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SEQUENCE 1232 AA; 136218 MW; 22688C662907C2D7 CRC64;
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 58; DB 4;
Pred. No. 1.6;
                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfam; PR00955; HCO3_cotranspt.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1064 KAVAPGDKPKIQEVKEQRV 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. Biophys. Res. Commun. 26
EMBL; U76669; AAP23240.1; -.
EMBL; U76667; AAP23240.1; JOINED.
EMBL; U76668; AAP23240.1; JOINED.
HSSP; P02730; 1BTQ.
                                                                                                        1059 KAVAPGDKPKIQEVKEQRV 1077
                                       7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5;
                                                                               2 KASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 KASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.48;
63.28;
60.4%;
ilarity 63.2%;
Conservative
                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1997 (TrEMBLrel. 03, 01-MAY-1997 (TrEMBLrel. 03, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                          Anion exchanger 2 type b2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGRFAMS; TIGRO0834; ae; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AE2 anion exchanger.
  Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-20090621;
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.2%; Score 54; DB 4; Length 357; 61.1%; Pred. No. 1.9; ive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 54; DB 4; Length 357; Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECUENCE FROM N.A.

TISSUE-Kidney;
Gebrig H., Appelhans H.;
Submitted (JAN-1993) to the EMBL/GenBank/DDBJ databases.
EMBL; X70797; CAA50067.1; -.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR03209; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotranspt.
PRINTS; PR01231; HCO3_TRNSPORT.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gehrig H.H., Yooenig J., Appelhans H.;
Gehrig H.H., Koenig J., Appelhans H.;
"Alternative anion exchange protein in human kidney.";
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
EMBL, X87211; CAA60670.1;
InterPro; IPR001717; Anion_exchange.
InterPro; IPR0030; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotranspt.
PROMISS, PROLIZ31; HCO3_TRNSPORT.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        357 AA; 39526 MW; 40C03D49F3AF359C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   357 AA; 39544 MW; DCB1FA569E19EEF0 CRC64;
                                                                                                                                              01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                        357 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               357 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anion exchange protein 3 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                        PRT;
                                                                                                                                                                                                                                Anion exchange protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       283 AIAPGDKPQIQEVREQRV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 ASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 ASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56.2%;
61.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 56.2
Best Local Similarity 61.1
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 61.1
Matches 11; Conservative
                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357
                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           013717;
                                                                                                                            099416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               013717
                                                                                                     099416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
Q13717
                                                        RESULT 14
Q99416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Medina J.F., Lecanda J., Acin A., Ciesielczyk P., Prieto J.; "Tissue-specific N-terminal isoforms from overlapping alternate promotèrs of the human AE2 anion exchanger gene."; Biochem. Biophys. Res. Commun. 267:228-235(2000). EMBL: U76669; AAF19583.2; ... EMBL: U76668; AAF19583.2; JOINED.
SEQUENCE FROM N.A.
MEDLINE=91179202; PubMed=9027488;
Medina J.F., Acin A., Prieto J.;
Molecular cloning and characterization of the human AE2 anion exchanger (SLC4A2) gene.";
Genomics 33:74-86(1997).
EMBL; U62531; AAC50964.1; -.
HSSP; P02730; 1BTQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=97179202; PubMed=9027488;
Medina J.F., Acin A., Prieto J.;
"Molecular cloning and characterization of the human AE2 anion exchanger (SLC4A2) gene.";
Genomics 39:74-85(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 58; DB 4; Length 1241;
Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 58; DB 4; Length 1241; Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGRRAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SEQUENCE 1241 AA; 136980 MW; D2FDA72E20D70D64 CRC64;
                                                                                                                                                                                                                                                                                                TIGRFAMS; TIGR00834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00210; ANION_EXCHANGER_2; 1.
SEQUENCE 1241 Aa; 137009 MW; D266ECDAB238FD97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1241 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR001717; Anion_exchange.
Interpro; IPR003020; HCO3_cotranspt.
Pfan; PF00955; HCO3_cotranspt.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                 InterPro, IPR001717; Anion_exchange.
InterPro, IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotransp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1073 KAVAPGDKPKIQEVKEQRV 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1073 KAVAPGDKPKIQEVKEQRV 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 KASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 KASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                              PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                       63.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.4%;
63.2%;
                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 63.2.
The 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anion exchanger 2 type a. SLC4A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-20090621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9UEY6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09UEY6
```

RESULT 13 Q9UEY6

g

δλ

ö

Gaps

ö

ó

Gaps

ö

Matches

g

δλ

283 ALAPGDKPOIQEVREORV 300

Search completed: September 3, 2003, 11:50:04 Job time : 45.5 secs Human erythrocyte
A. tigrinum AEI pr
Human erythrocyte
Human Band 3 prote

Novel human secret Mouse kidney cell A. tigrinum AE2 pr A. tigrinum AE3 pr Drosophila melanog Haemophilus influe

Haemophilus influe Haemophilus influe hNBC3 protein sequ hNBC3a protein sequ hNBC3 protein sequ Human brain-derive Murine Na+-driven

Human Na+-driven C Human transporter Human transporter Novel human diagno

Human secreted pro Human secreted pro glutamicum prote

Human secreted pro

Human heart muscle Human NT2-2A prote Rickettsia rickett Human Band 3 pepti Human Band 3 pepti Human ORFX protein

Human prostate can Amino acid sequenc A. orientalis gtfB

protein

Human AFP

Title: Perfect score:

Run on:

:sedneuce:

Scoring table:

Searched:

Database

```
Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine; protozoacide; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Band 3 polypeptide which selectively binds to merozite surface protein-1, useful for the prevention and treatment of malarial infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SELI-) ST ELIZABETH'S MEDICAL CENT INC
                      AAB46914
AAE29343
                                            AAE29344
AAU30825
AAP60645
AAW90262
AAW90261
                                                                                                   ABB63733
AAU35361
AAB88492
AAU91423
AAW74410
                                                                                                                                                           AAW74409
AAW74408
AAW74408
AAB47931
AAB47932
AAB47932
ABG32015
AAB232015
AAB28341
AAB28341
AAB28341
AAB28341
AAB28343
AAB90274
AAB02333
AAB02333
                                                                                                                                                                                                                                                                                                                                                                      AAG81363
AAB56872
AAW74715
AAY51558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu D, Goel V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE29340 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002; 2002WO-US06415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-MAR-2001; 2001US-272930P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Band 3 peptide, B35B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                       962.
10340
10340
10340
10330
10330
10444
1088
11106
11130
1130
                                                                                                                                                                                                                                                                                                               1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oh ss,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-759814/82
WO200270542-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chishti AH,
 AAE29340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE29340
  Human Band 3 pepti
Human Band 3 prote
Human liver peptid
Peptide #6645 enco
Protein #6029 enco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human brain expres
Human bone marrow
Peptide #6670 enco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human peptide enco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                           3, 2003, 11:24:37; Search time 48.5 Seconds (without alignments) 65.454 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                           A SIDISI/goddata/geneseqp-embl/AA1980.DAT:*

SIDISI/goddata/geneseqp-embl/AA1981.DAT:*

SIDISI/goddata/geneseqp-embl/AA1991.DAT:*

SIDISI/goddata/geneseqp-embl/AA1999.DAT:*

SIDISI/goddata/geneseqp-embl/AA1999.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                              1107863
            GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                       1107863 seqs, 158726573 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                        protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE29349
ABG54066
ABB39139
ABB24030
AAM59792
AAM72377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM32633
ABG42195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE29340
                                                                                                                                               1 SVTHANALTVMGKASTPGAA 20
                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                    A_Geneseq_19Jun03:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         П
                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                     US-10-087-464-2
98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyright
                                                                              September
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0
100.0
100.0
100.0
100.0
100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query
```

Score

Result Š. 888888888

25456780

```
sequence is human Band 3 protein ectoplasmic domain
                                                                                                                                                                                                                                                                                                                           ABG54066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sednence
                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
                                                                                                                                                                                                                                                  RESULT 3
ABG54066
 SXC
                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                  ö
                                               The invention relates to an isolated Band 3 polypeptide that comprises any of 4 20 residue amino acid sequences, or their fragments that bind to an MSPP-1 polypeptide or a polypeptide with any of 8 291.131 base pair sequences. The methods and compositions of the present invention are useful for the prevention and treatment of malarial infection. The present invention, develops new and more improved methods based upon inhibiting the particular interactions between the malarial parasite and a cognate molecule present in the host and subsequently minimising therapputic approaches. The invention is useful in gene therapy. The present invention also provides a vaccine for malaria. The present sequence is human Band 3 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated Band 3 polypeptide that comprises any of 4 20 residue amino acid sequences, or their fragments that bind to an MSP-1 polypeptide or a polypeptide with any of 8 291-1331 base pair sequences. The methods and compositions of the present invention are useful for the prevention and treatment of malarial infection. The present invention, develops new and more improved methods based upon inhibiting the particular interactions between the malarial parasite and a cognate molecule present in the host and subsequently minimising harmful side effects and drug resistance that may be due to non-specific therapeutic approaches. The invention is useful in gene therapy. The present invention also provides a vaccine for malaria. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine; protozoacide; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated Band 3 polypeptide which selectively binds to merozite surface protein-1, useful for the prevention and treatment of malarial
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                              Length 20;
                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                          100.0%; Score 98; DB 23; 100.0%; Pred. No. 1.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Band 3 protein ectoplasmic domain 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SELI-) ST ELIZABETH'S MEDICAL CENT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goel V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE29349 standard; peptide; 42 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example; Page 58; 163pp; English.
                 Claim 1; Page 84; 163pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                     20
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SVTHANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                     1 SVTHANALTVMGKASTPGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002; 2002WO-US06415,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-MAR-2001; 2001US-272930P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oh ss,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-759814/82
                                                                                                                                                                                                                                                                                                       20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200270542-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chishti AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infection
                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE29349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE29349
```

g

ò

```
ö
                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which human liver single exon encoded peptides of the invention.

Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for analysing gene expression in human adult liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 98; DB 22; 100.0%; Pred. No. 8.4e-09; Live 0; Mismatches 0;
                                               Score 98; DB 23;
Pred. No. 3.7e-09;
                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 27; SEQ ID No 32714; 658pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W, Rank DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human liver peptide, SEQ ID No 32714.
                                                                                                                                                                                                                                                                                                                                               ABG54066 standard; Peptide; 86 AA
                                                                                                                                                                                       12 SVTHANALTVMGKASTPGAA 31
                                                                                                                                                        1 SVTHANALTVMGKASTPGAA 20
                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC.
                                               100.08;
                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0207456.
2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001; 2001WO-US00664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0632366
2000US-0234687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0236359
2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-FEB-2003 (first entry)
                                    Ouery Match
Best Local Similarity 100.(
Matches 20, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-488898/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 20; Conserv
42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200157273-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-may-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2001
```

```
The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see Mas11852-Mas41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human brain expressed single exon probe encoded protein SEQ ID NO: 31897.
            Protein #6029 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                          Single exon nucleic acid probes for analyzing gene expression in human hearts -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
;
                                       Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 98; DB 22; 100.0%; Pred. No. 8.4e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 15; SEQ ID No 25800; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                 Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM59792 standard; Protein; 86 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SVTHANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVTHANALTVMGKASTPGAA
                                                                                                                                                                                                                                                                                                                                                                 Chen W,
                                                                                                                                                                                                                                                             2000US-0632366.
                                                                                                                                                                                                                                                                         21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                     30-JAN-2001; 2001WO-US00666
                                                                                                                                                                                                                                2000US-0207456
2000US-0608408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 20; Conservative
                                                                    congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                               Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 AA;
                                                                                                                             WO200157274-A2
                                                                                                                                                                                                               04-FEB-2000; 26-MAY-2000; 30-JUN-2000; 203-AUG-2000; 21-SEP-2000; 3
                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-NOV-2001
                                                                                                                                                          09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM59792;
                                                                                                                                                                                                                                                                                                                                                                 Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
AAM59792
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                              foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                  Peptide #6645 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 27; SEQ ID NO 31774; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 98; DB 22;
Pred. No. 8.4e-09;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB24030 standard; Protein; 86 AA
                                                                                                             ABB39139 standard; Peptide; 86 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
          SVTHANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45 SVTHANALTVMGKASTPGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SVTHANALTVMGKASTPGAA
                                                                                                                                                                                                                                                                                                                                                                                        26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0633366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
                                                                                                                                                                                                                                                                                                                                               30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-JAN-2002 (first entry)
                                                                                                                                                                   04-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 AA;
                                                                                                                                                                                                                                                                                     WO200157277-A2.
                                                                                                                                                                                                                                                           Homo sapiens.
                                     45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                         ABB39139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB24030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Penn SG,
                                                                                                                                                                                                                              Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
                                                                                 RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB24030
                                                                                               ABB39139
                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  £
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Z X X E
            õ
                                    g
```

```
probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for
                                                                                                                                                                                                      present invention provides a number of single exon nucleic acid
                                                                                                                   Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                  Example 4; SEQ ID NO: 32683; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide #6670 encoded by probe for measuring placental gene
                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 98; DB 22; Length 86; 100.0%; Pred. No. 8.4e-09; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder.
                                                                                                                                    analyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               analyzing gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 27; SEQ ID No 32902; 654pp; English.
                                               DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rank DR;
                                               Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                            1 SVTHANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                              SVTHANALTVMGKASTPGAA 64
               (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM32633 standard; Protein; 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC
                                               Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen W,
                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.0%;
Matches 20; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0236359
2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanzel DK,
                                               Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-488897/53
                                                                                 WPI; 2001-488900/53
                                                                                                                                                                                                                                                                                                                         86 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200157272-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Penn SG,
                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM32633;
                                                                                                                                                                                                                                                                                                                                                           Query Match
                                               Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KESULT 8
AAM32633
                                                                                                                                                                                                        The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple scierosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                                                                                                                                                                         Single exon nucleic acid probes for analyzing gene expression in human brains -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human bone marrow expressed probe encoded protein SEQ ID NO: 32683.
                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; SEQ ID NO: 31897; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 98; DB 22; 100.0%; Pred. No. 8.4e-09;
                                                                                                                                                                                                                                                                                           Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 SVTHANALTVMGKASTPGAA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SVTHANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86
                                                                                                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                           Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0632366.
2000US-0234687.
2000US-0236359.
2000GB-0024263.
                                                                                                                                               30-JUN-2000; 2000US-060B40B.
13-NUG-2000; 2000US-0632566.
21-SEP-2000; 2000US-0235559.
27-SEP-2000; 2000US-0235559.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM72377 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0207456.
2000US-0608408.
                                                                                 2001WO-US00667
                                                                                                                   2000US-0180312
                                                                                                                                    2000US-0207456
2000US-0608408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20; Conservative
                                                                                                                                                                                                                                                                                         Hanzel DK,
                                                                                                                                                                                                                                                                                                                       WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 AA;
              WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200157276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001;
                                                                                 30-JAN-2001;
                                                                                                                 04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAY-2000;
30-JUN-2000;
                                                                                                                                    26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-NOV-2001
                                              09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM72377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                         Penn SG,
```

Matches

δ q

AAM7237 RESULT

expression.

:, 0

Gaps

```
RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR15355
   Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with mRNA, and (b) measuring the label detectably bound to each probe of
predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                           Human peptide encoded by genome-derived single exon probe SEQ ID 31860.
                                                                                                                                                                                                                                                                                                                                             Permansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples -
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                 Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic Obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                               ö
                                                                      Length 86;
                                                                                               Indels
                                                                      100.0%; Score 98; DB 22;
100.0%; Pred. No. 8.4e-09;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 27; SEQ ID No 31860; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rank DR;
                                                                                                                                                                                                      ABG42195 standard; Peptide; 86 AA
                                                                                                                      1 SVTHANALTVMGKASTPGAA 20
                                                                                                                                    45 SVTHANALTVMGKASTPGAA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0632366.
2000US-234687P.
2000US-236359P.
2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-207456P.
2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2001; 2001WO-US00665.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-180312P
                                                                                                                                                                                                                                                    (first entry)
                                                                                  Local Similarity 100.
nes 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    primary ciliary dyskinesi
hyaline membrane disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-114183/15.
                                                86 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200186003-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                    19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-NOV-2001
                                                                                                                                                                                                                              ABG42195;
                                                 Sequence
                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Penn SG,
                                                                                               Matches
                                                                                                                                                                               RESULT 9
ABG42195
                                                                                                                                                                                                                              ប្តូប្តូប្តី នូ
                                                                                                                      ò
                                                                                                                                            a
```

```
the array; identifying exons in a eukaryotic genome, comprising

(a) algorithmically predicting at least one exon from genomic sequences
of the eukaryote; and (b) detecting specific hybridisation of detectably
labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
having a fragment identical to the predicted exon, the probe is included
in the above mentioned microarray; assigning exons to a single gene,
comprising (a) identifying exons from genomic sequence by the method
above and (b) measuring the expression of each of the exons in several
tissues and/or cell types using hybridisation to a single exon
microarrays having a probe with the exon, where a common pattern of
expression of the exons in the tissues and/or cell types indicates that
the exons should be assigned to a single gene; a peptide comprising one
of 12011 sequences, mentioned in the specification, or encoded by the
probes/open reading frames (ORF). The probes are used for gene
probes/open reading frames (ORF). The probes are used for gene
expression analysis, and for identifying exons in a gene, particularly
using human lung derived mRNA and for the study of lung disease
copins hierstitial lung disease (ILD), familial idiopathic pulmonary
librosis, neurofibromatosis, tubercus sclerosis, Gaucher's disease,
Niemann-Pick disease, Hermansky-Pudlask syndrome, fibrocystic
pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic
pulmonary alveolar proteinosis, Karagener syndrome, incordial purposed the present sequence is a peptide/protein
encoded by a single exon probe of the invention.

Company and the sexon probe of the invention of forming a peptide/protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic senescent cell antigen and peptide(s) - used to detect antibodies to SCA, study cellular ageing and auto-immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human erythrocyte membrane anion-transport protein (band 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Senescent cell peptide; ANION 1; COOH; auto immune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 98; DB 23;
100.0%; Pred. No. 8.4e-09;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (RESE ) RESEARCH CORP TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR15355 standard; Protein; 911 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SVTHANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 SVTHANALTVMGKASTPGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90US-0528210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91WO-US03557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marchalonis JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1991-369184/50.
N-PSDB; AAQ15172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-NOV-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
08-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9118013-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        кау мвм,
```

9

Wed Sep

us-10-087-464-2.rag

```
The amino acid sequence is that of the human erythrocyte anion-transport protein (band 3). Amino acids 538-554 (ANION 1) or 812-827 (COCH) code for a peptide which is immuno-reactive with antibodies to senescent cell artigen (SCA). The antigen and peptides can be used in any method or technique involving or requiring the inhibition of the binding of senescent cells in vitro or in vivo. The prods. Can be used in to examine various physiological, biochemical, and immunological mechanisms in humans and other animals, such as those including to cellular ageing, degeneration, and life span; removal of senescent cells; anion transport across cellular membranes; disease mechanisms where increased senescent cell IgG may play a role, such as rhoundary and semilytic anemial, sickle cell anaemia, and idiopathic thrombocytopenia purpura; other autoimmune disease mechanisms, such as rhoundary and strike cell anaemia, and cancer. More structured arthritis and systemic lupus erythematosus; and other specifically, the prods. are useful in cosmetic and pharmaceutical compsns., diagnostic kits, and methods for detecting or measuring separating anions from a gas or liquid, or diagnosis and treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NBC; sodium bicarbonate transporter family; pH regulation; immunoassay; treatment; water retention; blood pressure; acidosis; inflammation; cell proliferation; cancer; sperm activation; inactivation; epilepsy; hydroencephaly; glaucoma; colitis; salamander; AEI; anion exchange.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bevensee MO, Biemesderfer D, Boron WF; is BA, Grichtchenko II, Romero MF, Schmitt BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 98; DB 12; Length 911; 100.0%; Pred. No. 1.3e-07; 1ve 0; Mismatches 0; Indels (
mechanisms, separate anions and treat auto-immune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                 (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW90263 standard; peptide; 911 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   731 SVTHANALTVMGKASTPGAA 750
                                   Disclosure; Fig 1; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SVTHANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-US10297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0047131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A. tigrinum AE1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aalkjaer C, Bevense
مئمن I. Davis BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-059743/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ambystoma tigrinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYYA ) UNIV YALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9853067-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sussman CR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW90263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW90263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
```

New nucleic acid molecules encoding proteins of the Sodium Bicarbonate Cotransporter (NBC) family - useful for identifying agents that agonise or antagonise NBC activity and treating

ö

Gaps

ö

```
a method resulting in the isolation of a novel salamander sodium bicarbonate transporter (NBC). NBC proteins and nucleic acid sequences may be used to treat pathological processes including water retention, increased blood pressure, chronic respiratory and metabolic acidosis, inflammation, cell proliferation, cancer, sperm activation/inactivation, hydroencephaly, epilepsy, glaucoma and colitis. Members of the NBC family of proteins can be used (i) as a target to identify agents that block or stimulate NBC mediated pH regulation, (ii) as a target to bait to identify agents that block or stimulate activity of an NBC protein, and identify agents that block or stimulate activity of an NBC protein, and (iv) as a target to assay for NBC-mediated activity. Anti-NBC antibodies are also useful as modulators of NBC activity, useful in the immunoassays for detecting NBC expression/activity and for purifying an NBC protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Erythrocyte band 3 anion transporter protein; human; hypercoagulation; iron-nitrosyl hemoglobin; electron paramagnetic resonance; UV spectra; EPR; nitric oxide; antianemic; antibacterial; immunosuppressive; vasotropic; antilnflammatory; antiasthmatic; respiratory; antiarthritic; cerebroprotective; red blood cell membrane defect; vasculopathy; espectic shock mycoardial depression; pancreatitis; sickle cell crisis; urinary tract infection; progressive respiratory failure; septicemia; ischemia; arthritis; asthma; cerebritis; bronchitis; vasculitis.
                                                                              This sequence represents the anion exchange protein AE1 which is used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel method for determining the predominant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Determining predominant physiological effect of composition comprising hemoglobin used to produce methods of therapy for medical disorders by using EPR or UV spectra of iron nitrosyl hemoglobin derivatives -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 98; DB 20; Length 911; 100.0%; Pred. No. 1.3e-07; tive 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human erythrocyte band 3 anion transporter protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB46914 standard; protein; 911 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              731 SVTHANALTVMGKASTPGAA 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 11; 70pp; English.
                                        Example 1; Fig 5; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SVTHANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Singel DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-AUG-2000; 2000WO-US21101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0146680.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (RERE-) RES & DEV INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
disorders mediated by NBC
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stamler JS, Gow AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-183002/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYDU-) UNIV DUKE.
                                                                                                                                                                                                                                                                                                                                                                                   911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200109616-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB46914;
                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB46914
쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
```

```
involves obtaining electron paramagnetic resonance (EPR) or UV spectra of involves obtaining electron paramagnetic resonance (EPR) or UV spectra of intricoxide (NO) with hemoglobin and determining if the composition shows non-cooperativity or cooperativity in binding of NO to the hemoglobin. The products of the invention have antianemic; antibacterial; mmunosuppressive; vasotropic; antiinflammatory; antiasthmatic; respiratory; antiarthritic and cerebroprotective activity. The products of the invention are used to produce methods of therapy for medical disorders characterized by red blood cell membrane defects and for a variety of hypercoaquiable and vasculopathic states, particularly for patients with septic shock who develop myocardial depression, parients with septic shock who develop myocardial depression, parients with septicemia as a complication of urinary tract infection and patients with schemia, patients in a sickle cell crisis and for treating inflammatory conditions such as arthritis, asthma, cerebritis, bronchitts and vasculitis. The methods are also used for preserving red blood cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated Band 3 polypeptide that comprises any of 4.20 residue amino acid sequences, or their fragments that bind to an MSP-1 polypeptide or a polypeptide with any of 8 291-1331 base pair sequences. The methods and compositions of the present invention are useful for the prevention and treatment of malarial infection. The present invention, develops new and more improved methods based upon inhibiting the particular interactions between the malarial parasite and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide; malarial infection; drug resistance; vaccine; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated Band 3 polypeptide which selectively binds to merozite surface protein-1, useful for the prevention and treatment of malarial infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
physiological effect of a composition comprising hemoglobin which
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                          Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 98; DB 22;
100.0%; Pred. No. 1.3e-07;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 102-105; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SELI-) ST ELIZABETH'S MEDICAL CENT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goel V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE29343 standard; Protein; 911 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SVTHANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                which can be used in therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002; 2002WO-US06415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAR-2001; 2001US-272930P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.
nes 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Band 3 protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chishti AH, Oh SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002-759814/82.
                                                                                                                                                                                                                                                                                                                                                                      911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAD46978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200270542-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; Band 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protozoacide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE29343;
                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE29343
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated Band 3 polypeptide that comprises any of 4 20 residue amino acid sequences, or their fragments that bind to an MSP-1 polypeptide or a polypeptide with any of 8 291-131 base pair sequences. The methods and compositions of the present invention are useful for the prevention and treatment of malarial infection. The present invention, develops new and more improved methods based upon inhibiting the particular interactions between the malarial parasite and a cognate molecule present in the host and subsequently minimising harmful side effects and drug resistance that may be due to non-specific, therapeutic approaches. The invention is useful in gene therapy. The present invention also provides a vaccine for malaria. The present sequence is human Band 3 protein.
a cognate molecule present in the host and subsequently minimising harmful side effects and drug resistance that may be due to non-specific therapeutic approaches. The invention is useful in gene therapy. The present invention also provides a vaccine for malaria. The present sequence is human Band 3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine; protozoacide; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated Band 3 polypeptide which selectively binds to merozite surface protein-1, useful for the prevention and treatment of malarial infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                      Gaps
                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                     Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 911;
                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 98; DB 23;
100.0%; Pred. No. 1.3e-07;
Live 0; Mismatches 0;
                                                                                                                                   Score 98; DB 23;
Pred. No. 1.3e-07;
                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 107-110; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SELI-) ST ELIZABETH'S MEDICAL CENT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goel V;
                                                                                                                                                                                                                                                                                                                      AAE29344 standard; Protein; 911 AA
                                                                                                                                                                                                                      731 SVTHANALTVMGKASTPGAA 750
                                                                                                                                                                                                     20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SVTHANALTVMGKASTPGAA 20
                                                                                                                                 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 20; Conservative 0;
                                                                                                                                                                                                   1 SVTHANALTVMGKASTPGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002; 2002WO-US06415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAR-2001; 2001US-272930P
                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       Human Band 3 protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-759814/82.
N-PSDB; AAD46979.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oh ss,
                                                                                                    911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200270542-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                        27-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chishti AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-SEP-2002
                                                                                                                                                                                                                                                                                                                                                       AAE29344;
                                                                                                      Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                       RESULT 14
                                                                                                                                                                                                                                                                                                      AAE29344
   8888888
                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                     ŏ
```

```
The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for polypeptides and antibodies to the polypeptides are useful for with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and the rest proteins are useful in genetic vaccination, testing and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopolesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAUS510-AAU3304 represent the amino acid in treatment of leukaemias. AAUS510-AAU3304 represent the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
                                                                                                                                                                                                                                                                Human; vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 98; DB 22; 100.0%; Pred. No. 1.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                           Novel human secreted protein #1316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; Page 354; 765pp; English.
                                                                                                             AAU30825 standard; Protein; 962 AA
Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-APR-2001; 2001WO-US08656.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-APR-2000; 2000US-0552929.
26-JAN-2001; 2001US-0770160.
                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-611725/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      962 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                            WO200179449-A2.
                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                      18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                 25-OCT-2001.
                                                                                                                                                    AAU30825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                        RESULT 15
                   g
```

ö

ö

Search completed: September 3, 2003, 11:46:11 Job time : 48.5 secs

1 SVTHANALTVMGKASTPGAA 20

g à

Human erythrocyte

911 12 AAR15355

100.0

```
96
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                        7; Search time 48.5 Seconds (without alignments) 65.454 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A_ceneseq_150 unto;

1. (SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT;*

2. (SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT;*

3. (SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT;*

3. (SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT;*

3. (SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT;*

3. (SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT;*

3. (SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT;*

3. (SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT;*

4. (SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT;*

5. (SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT;*

5. (SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT;*

5. (SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT;*

5. (SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT;*

5. (SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT;*

5. (SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT;*

5. (SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT;*

5. (SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT;*

5. (SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT;*

5. (SIDS1/gcgdata/geneseq/g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1107863
                                      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1107863 segs, 158726573 residues
                                                                                                                                                                                                                                                                                                             3, 2003, 11:24:37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GKASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A_Geneseq_19Jun03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-087-464-3
96
                                                                                                                                                                                                                                                                                                             September
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
                                                                                                                                                                                                                                                                                                             Run on:
```

SUMMARIES

		æ				
Result		Query				
No.	Score	Match I	Match Length DB	0 B	ID	Description
	96	100.0	20	23	AAE29341	Human Band 3 pepti
? ; •	96	100.0	42	23	AAE29349	Human Band 3 prote
ო	96	100.0	98	22	ABG54066	. Human liver peptid
	96	100.0	98	22	ABB39139	Peptide #6645 enco
5	96	100.0	86	22	ABB24030	Protein #6029 enco
9	96	100.0	98	22	AAM59792	Human brain expres
7	96	100.0	98	22	AAM72377	Human bone marrow
80	96 .	100.0	98	22	AAM32633	Peptide #6670 enco
σ	96	100.0	98	23	ABG42195	Human peptide enco

THE STATE OF THE S	AAM12359 Humman Erytm AAM90263 Human Erytm AAB46914 Human Erytm AAE29343 Human Erytm AAE29344 Human Band AAU30825 Novel human AAP60645 Movel human AAW90265 A tioney	AAW90261 AAE29340 AAE29340 AAE11308 AAB60494 ABB62013 AAU7822 AAU7094 AAR57771 ABB63733 AAR49667	21 AAG02687 Human secreted proposed	ide; 20 AA. ry) ise; malarial infection; drug resistance; vaccine;	USO6415. 272930P. 'S MEDICAL CENT INC. Liu D, Goel V; polypeptide which selectively binds to merozite
11 12 13 14 15 16 17 18 18 18 19 10 10 10 10 10 11 11 11 12 13 14 14 14 14 14 14 14 14 14 14	0 9111 0 9111 0 9111 0 962 4 1282 1280	1039 1039 1039 1039 1039 1039 1039 1039	.8 264 .8 264 .8 1162 .8 1162 .8 1185 .8 1296 .8 2379 .8 2379 .7 85	; peptid st entry ide, B35 ypeptide	, , = ,
	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2) N 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	WWWWWWWWWWWWWWWWWWWWWWWW	11 1E29341 stan EE29341; -JAN-2003 uman Band 3 :ctczoacide; omo sapiens.	

ö

42 AA;

ò g

```
sequence is human Band 3 protein ectoplasmic domain 5.
                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG54066
                                                                                                                                                                                                                                              Oy .
SXC
                                                                                                                                                                                                                                                                                                               엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                             any of 4.20 residue amino acid sequences, or their fragments that bind to an MSP-1 polypeptide or a polypeptide with any of 8 291-1331 base pair sequences. The methods and compositions of the present invention are useful for the prevention and treatment of malarial infection. The present invention, develops new and more improved methods based upon inhibiting the particular interactions between the malarial parasite and cognate molecule present in the host and subsequently minimising therapeutic approaches. The invention is useful in gene therapy. The present invention also provides a vaccine for malaria. The present sequence is human Band 3 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated Band 3 polypeptide that comprises any of 4 20 residue amino acid sequences, or their fragments that bind to an MSPP-1 polypeptide or a polypeptide with any of 8 291.131 base pair sequences. The methods and compositions of the present invention are useful for the prevention and treatment of malarial infection. The present invention, develops new and more improved methods based upon inhibiting the particular interactions between the malarial parasite and a cognate molecule present in the host and subsequently minimising a cognate molecule present in the host and subsequently minimising therapoutic approaches. The invention is useful in gene therapy. The present invention also provides a vaccine for malaria. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine; protozoacide; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated Band 3 polypeptide which selectively binds to merozite surface protein-1, useful for the prevention and treatment of malarial infection
                                                                                       The invention relates to an isolated Band 3 polypeptide that comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 96; DB 23; 100.0%; Pred. No. 2.4e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Band 3 protein ectoplasmic domain 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ST ELIZABETH'S MEDICAL CENT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goel V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE29349 standard; peptide; 42 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 84; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example; Page 58; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002; 2002WO-US06415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-MAR-2001; 2001US-272930P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chishti AH, Oh SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-759814/82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200270542-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE29349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SELI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
AAE29349
```

THE STATE OF THE S

```
The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is associated with coronary heart disease. ABG47348-ABG59930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                         Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analysing gene expression in human adult liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 86;
   Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 96; DB 22; ilarity 100.0%; Pred. No. 1.3e-08; Conservative 0; Mismatches 0;
; Score 96; DB 23;
; Pred. No. 5.6e-09;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 27; SEQ ID No 32714; 658pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen W, Rank DR;
                                                                                                                                                                                                                                                                             Human liver peptide, SEQ ID No 32714.
                                                                                                                                                                                 ABG54066 standard; Peptide; 86 AA
                                                                                     23 GKASTPGAAAQIQEVKEQRI 42
                                                                  1 GKASTPGAAQIQEVKEORI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC.
   100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US00664
                                                                                                                                                                                                                                             25-FEB-2003 (first entry)
                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-488898/53
   Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                         WO200157273-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                         09-AUG-2001
                                                                                                                                                                                                                 ABG54066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
```

3

δλ a

```
The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA11535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human brain expressed single exon probe encoded protein SEQ ID NO: 31897.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
             Protein #6029 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                  Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 96; DB 22; Length 86; 100.0%; Pred. No. 1.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 15; SEQ ID No 25800; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM59792 standard; Protein; 86 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GKASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 GKASTPGAAAOIOEVKEORI 75
                                                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                       2000US-0180312.
2000US-0207456.
2000US-0608408.
                                                                                                                                                                                                                                    30-JAN-2001; 2001WO-US00666
                                                                                                                                                                                                                                                                                                                                              2000US-0234687
2000US-0236359
                                                                                                                                                                                                                                                                                                                                                                                     2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 100.
Matches 20; Conservative
                                                                                      congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 AA;
                                                                                                                                                           WO200157274-A2.
                                                                                                                                                                                                                                                                     04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                              21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                     04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-NOV-2001
                                                                                                                                                                                                  09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM59792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hearts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM59792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВÞ
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                        Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                      Peptide #6645 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 27; SEQ ID NO 31774; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 96; DB 22;
100.0%; Pred. No. 1.3e-08;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ą
                                                                                                                                        ABB39139 standard; Peptide; 86 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GKASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB24030 standard; Protein; 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen W,
             GKASTPGAAAQIQEVKEQRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 2000us-0180312.
; 2000us-0207456.
; 2000us-0608408.
; 2000us-053236.
; 2000us-0234687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-OCT-2000; 2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-JAN-2002 (first entry)
                                                                                                                                                                                                             04-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-483447/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 AA;
                                                                                                                                                                                                                                                                                                                                                              WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
                                                                                                                                                                             ABB39139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB24030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
ABB24030
                                                                                                                         ABB39139
                                                                                                     RESULT
```

ò g HXXX H

```
The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide #6670 encoded by probe for measuring placental gene expression.
                                                                                                          Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                        Example 4; SEQ ID NO: 32683; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                              100.0%; Score 96; DB 22;
100.0%; Pred. No. 1.3e-08;
Live 0; Mismatches 0;
                                                                                                                            analyzing gene expression in human bone marrow
                                           Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ¥.
                                                                                                                                                                                                                                                                                                                                                                                               1 GKASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM32633 standard; Protein; 86
             (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0632366.
2000US-0234687.
2000US-0236359.
2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0207456.
2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Penn SG, 'Hanzel DK,
                                            Hanzel DK,
                                                                         WPI; 2001-488900/53
                                                                                                                                                                                                                                                                                                                                             Local Similarity
es 20; Conserv
                                                                                                                                                                                                                                                                                                  86 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200157272-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAY-2000,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM32633;
                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                              Query Match
                                            Penn SG,
                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
g
                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                          probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple scherosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                                                                                                                                              Single exon nucleic acid probes for analyzing gene expression in human brains \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human bone marrow expressed probe encoded protein SEQ ID NO: 32683.
                                                                                                                                                                                                                                                                                                                                                                           Example 4; SEQ ID NO: 31897; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 96; DB 22; 100.0%; Pred. No. 1.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                  Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM72377 standard; Protein; 86 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GKASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                   04-FEB-2000; 2000US-0180312.
26-MX-2000; 2000US-0207456.
30-UN-2000; 2000US-068408.
03-AUG-2000; 2000US-0532366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234559.
04-OCT-2000; 2000US-0236359.
                                                                                                                                                                                                                                                                 Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0236359.
2000GB-0024263.
                                                                         2001WO-US00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20; Conservative
                                                                                                                                                                                                                                                                 Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                               WPI; 2001-483446/52
         WO200157275-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200157276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
                                                                         30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-NOV-2001
                                         09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM72377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM7237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
```

ò ద

ö

ö

Length 86; Indels

```
The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for
Human genome-derived single exon nucleic acid probes useful for
                                                           analyzing gene expression in human placenta
                                                                                                                                                                     Claim 27; SEQ ID No 32902; 654pp; English.
```

888666

a ò

S

```
RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR15,355
     δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with mRNA, and (b) measuring the label detectably bound to each probe of
predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                             Human peptide encoded by genome-derived single exon probe SEQ ID 31860.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hermansky-Pudlak syndrome; sarcoldosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         {\tt Spatially-addressable} set of single exon nucleic acid probes, used to measure gene expression in human lung samples -
                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                       ö
                                                                                                     Length 86;
                                                                                                                                       Indels
                                                                                                    100.0%; Score 96; DB 22;
100.0%; Pred. No. 1.3e-08;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27; SEQ:ID No 31860; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen W, Rank DR;
                                                                                                                                                                                                                                                                                         ABG42195 standard; Peptide; 86 AA.
                                                                                                                                                                        1 GKASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-207456P.
2000US-0608408.
2000US-0632366.
2000US-234687P.
2000US-236359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-2001; 2001WO-US00665
                                                                                                                                                                                                                                                                                                                                                          19-AUG-2002 (first entry)
                                                                                                                    Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-114183/15.
                                                                    86 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200186003-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-NOV-2001
                                                                                                                                                                                                                                                                                                                          ABG42195;
                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Penn SG,
                                                                                                     Query Match
                                                                                                                                                                                                                                                         RESULT 9
ABG42195
```

```
the array; Identitying exons in a eutaryour yencome, computating

(a) algorithmically predicting at least one exon from genomic sequences

(c) the eukaryote; and (b) detecting specific hybridisation of detectably

(a) babled nucleic acids from eukaryote lung mRNA, to a single exon probe,

(c) labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,

(c) having a fragment identical to the predicted exon, the probe is included

(d) measuring the expression of each of the exons in several

(c) comprising (a) identifying exons from genomic sequence by the method

(c) microarrays having a probe with the exon, where a common pattern of

(c) microarrays having a probe with the exon, where a common pattern of

(c) the exons should be assigned to a single gene; a peptide comprising one

(c) the exons should be assigned to a single gene; a peptide comprising one

(c) the exons should be assigned to a single gene; a peptide comprising one

(c) the exons should be assigned to a single gene; a peptide comprising one

(c) the exons should be assigned to a single gene; a peptide comprising one

(c) the exons should be assigned to a single gene; a peptide comprising one

(c) the exons should be assigned to a single gene; a peptide comprising one

(c) the exons should be assigned to a single gene; a gene;

(c) the exons should be assigned to a single gene; a gene;

(c) the exons should be assigned to a single gene;

(c) the exons should defines (ORF). The probes, pulmonary diseases

(c) the exons should define the specification, or encoded by the present syndrome, sarcoidosis, pulmonary hypertension

(c) the exons are the exon probe of the invention.

(c) the exons are the exon probe of the invention.

(c) the exons are the exon probe of the invention.

(c) the exons are the exon probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic senescent cell antigen and peptide(s) - used to detect antibodies to SCA, study cellular ageing and auto-immune
array; identifying exons in a eukaryotic genome, comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human erythrocyte membrane anion-transport protein (band 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 96; DB 23; Length 86; 100.0%; Pred. No. 1.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Senescent cell peptide; ANION 1; COOH; auto immune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (RESE ) RESEARCH CORP TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR15355 standard; Protein; 911 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GKASTPGAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91WO-US03557.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90US-0528210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kay MBM, Marchalonis JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (nbdated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1991-369184/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAQ15172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
08-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-NOV-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9118013-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
```

```
The amino acid sequence is that of the human erythrocyte anion-transport protein (band 3). Amino acids 588-554 (ANION 1) or 812-827 (COCH) code for a peptide which is immuno-reactive with antibodies to senescent cell antigen (SCA). The antigen and peptides can be used in any method or technique involving or requiring the inhibition of the binding of senescent cells in vitro or in vivo. The prods. Can be used in to examine various physiological, biochemical, and immunological mechanisms in humans and other animals, such as those relating to cellular ageing, degeneration, and life span; removal of senescent cells; anion transport across cellular membranes; disease mechanisms where increased senescent cell IgG may play a role, such as homocytopenia purpura; other autoimmune disease mechanisms, such as rheumatoid arthritis and systemic lupus erythematosus; and other diseases such as those involved in malaria and cancer. More specifically, the prods are useful in cosmetic and pharmaceutical compsns., diagnostic kits, and methods for detecting or measuring has such diseases.

Separating anions from a gas or liquid, or diagnosis and treatment contraction diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NBC; sodium bicarbonate transporter family; pH regulation; immunoassay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treatment; water retention; blood pressure; acidosis; inflammation; cell proliferation; cancer; sperm activation; inactivation; epilepsy; hydroencephaly; glaucoma; colitis; salamander; ABI; anion exchange.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid molecules encoding proteins of the Sodium Bicarbonate Cotransporter (NBC) family - useful for identifying agents that agonise or antagonise NBC activity and treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bevensee MO, Biemesderfer D, Boron WF;
Is BA, Grichtchenko II, Romero MF, Schmitt BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 911;
 mechanisms, separate anions and treat auto-immune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 96; DB 12; 100.0%; Pred. No. 1.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                 (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW90263 standard; peptide; 911 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 1; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GKASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-US10297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0047131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A. tigrinum AE1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aalkjaer C, Bevense
Choi I, Davis BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-059743/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ambystoma tigrinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYYA') UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9853067-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sussman CR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW90263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ద
```

```
ö
                                                             This sequence represents the anion exchange protein AEI which is used in a method resulting in the isolation of a novel salamander sodium bicarbonate transporter (NBC). NC proteins and nucleic acid sequences may be used to treat pathological processes including water retention, increased blood pressure, chronic respiratory and metabolic acidosis, inflammation, cell proliferation, cancer, sperm activation/inactivation, bydroencephaly, epilepsy, glaucoma and colitis. Members of the NBC family of proteins can be used (1) as a target to identify agents that block or stimulate activity of an NBC protein, and identify and isolate binding partners that blod NBC, (111) in methods to identify agents that block or stimulate activity of an NBC protein, and it is a starget to assay for NBC-mediated activity, useful in the immunoassays for detecting NBC expression/activity and for purifying an NBC protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             iron-nitrosyl hemoglobin; electron paramagnetic resonance; UV spectra;
EPR; nitric oxide; antianemic; antibacterial; immunosuppressive;
vasotropic; antiinflammatory; antiasthmatic; respiratory; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel method for determining the predominant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Determining predominant physiological effect of composition comprising hemoglobin used to produce methods of therapy for medical disorders by using EPR or UV spectra of iron nitrosyl hemoglobin derivatives -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Erythrocyte band 3 anion transporter protein; human; hypercoagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cerebroprotective; red blood cell membrane defect; vasculopathy; septic shock myocardial depression; pencreatitis; sickle cell crisis; urinary tract infection; progressive respiratory failure; septicemia; ischemia; arthritis; asthma; cerebritis; bronchitis; vasculitis.
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                      Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human erythrocyte band 3 anion transporter protein.
                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                      Score 96; DB 20;
Pred. No. 1.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB46914 standard; protein; 911 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 11; 70pp; English
                                  Example 1; Fig 5; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GKASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Singel DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                           ;
;
                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-AUG-2000; 2000WO-US21101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0146680.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (RERE-) RES & DEV INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 100.0
Matches 20, Conservative
disorders mediated by NBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GOW AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-183002/18
                                                                                                                                                                                                                                                                                                                                                 911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYDU-) UNIV DUKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200109616-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stamler JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38-FEB-2001
                                                                                                                                                                                                                                                                                                                                                     Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB46914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB46914
qq
```

```
involves obtaining electron paramagnetic resonance (EPR) or UV spectra of intricosyl hemoglobin derivatives formed by incubation of limiting nitric oxide (No) with hemoglobin and determining if the composition shows non-cooperativity or cooperativity in binding of No to the hemoglobin. The products of the invention have antianemic; antibacterial; immunosuppressive; vasotropic; antiinflammatory; antiasthmatic; respiratory; antiarthritic and cerebroprotective activity. The products of the invention are used to produce methods of therapy for medical disorders characterized by red blood cell membrane defects and for a variety of hypercoaquiable and vasculopathic states, particularly for patients with septic shock who develop myocardial depression, pancreatitis and progressive respiratory failure, patients with septic shock who develop myocardial depression, concreatitis and progressive respiratory failure, patients with sischemia, patients in a sickle cell crisis and for treating inflammatory conditions such as arthritis, asthma, cerebritis, bronchitis and vasculation or products of the products of the methods are also used for preserving red blood cells
                                                                                                                                                                                                                                                                                                                                                                                                                                            ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated Band 3 polypeptide that comprises any of 4 20 residue amino acid sequences, or their fragments that bind to an MSP-1 polypeptide or a polypeptide with any of 8 291-1331 base pair sequences. The methods and compositions of the present invention are useful for the prevention and treatment of malarial infection. The present invention, develops new and more improved methods based upon inhibiting the particular interactions between the malarial parasite and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide; malarial infection; drug resistance; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Band 3 polypeptide which selectively binds to merozite surface protein-1, useful for the prevention and treatment of malarial
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
physiological effect of a composition comprising hemoglobin which
                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                    Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 96; DB 22; 100.0%; Pred. No. 1.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 102-105; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SELI-) ST ELIZABETH'S MEDICAL CENT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goel V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE29343 standard; Protein; 911 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GKASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                            which can be used in therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAR-2001; 2001US-272930P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002; 2002WO-US06415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Band 3 protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chishti AH, Oh SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002-759814/82.
                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAD46978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200270542-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protozoacide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Band
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE29343;
                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human;
                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE29343
$$$$$$$$$$$$$$$$$$$$$$$$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

```
ö
                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      any of 4 20 residue amino acid sequences, or their fragments that bind to an MSP-1 polypeptide or a polypeptide with any of 8 291-1331 base pair sequences. The methods and compositions of the present invention are useful for the prevention and treatment of malarial infection. The present invention, develops new and more improved methods based upon inhibiting the particular interactions between the malarial parasite and a cognate molecule present in the host and subsequently minimising harmful side effects and drug resistance that may be due to non-specific
              harmful side effects and drug resistance that may be due to non-specific therapeutic approaches. The invention is useful in gene therapy. The present invention also provides a vaccine for malaria. The present sequence is human Band 3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine; protozoacide; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated Band 3 polypeptide which selectively binds to merozite surface protein-1, useful for the prevention and treatment of malarial infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated Band 3 polypeptide that comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapeutic approaches. The invention is useful in gene therapy. The present invention also provides a vaccine for malaria. The present sequence is human Band 3 protein.
cognate molecule present in the host and subsequently minimising
                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 911;
                                                                                                                                    Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                  Indels
                                                                                                                                                              0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 96; DB 23;
100.0%; Pred. No. 1.8e-07;
ive 0; Mismatches 0;
                                                                                                                                  Score 96; DB 23;
Pred. No. 1.8e-07;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 107-110; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SELI-) ST ELIZABETH'S MEDICAL CENT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goel V;
                                                                                                                                                                                                                                                                                                                         ¥.
                                                                                                                                                                                                                     742 GKASTPGAAAQIQEVKEQRI 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GKASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                     1 GKASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                        AAE29344 standard; Protein; 911
                                                                                                                                Match 100.0%; S. Local Similarity 100.0%; P. P. les 20; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002; 2002WO-US06415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAR-2001; 2001US-272930P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          Human Band 3 protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-759814/82.
N-PSDB; AAD46979.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oh ss,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 911 AA;
                                                                                                  911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200270542-A2.
                                                                                                                                                                                                                                                                                                                                                                                           27-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chishti AH,
                                                                                                                                                                                                                                                                                                                                                         AAE29344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
                                                                                                    Sequence
                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ното
                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                        RESULT 14
                                                                                                                                                                                                                                                                                                          AAE29344
                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
8888888
                                                                                                                                                                                                       οy
                                                                                                                                                                                                                                   g
```

```
The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopolesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bone, cartilage, tendon and/or nerve tissue growth or regeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 96; DB 22;
100.0%; Pred. No. 1.9e-07;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; Page 354; 765pp; English.
                                                                                                                                                                                                                                 AAU30825 standard; Protein; 962 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human secreted protein #1316.
742 GKASTPGAAAQIQEVKEQRI 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-APR-2000; 2000US-0552929.
26-JAN-2001; 2001US-0770160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-APR-2001; 2001WO-US08656.
                                                                                                                                                                                                                                                                                                                                                                                      18-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 20, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-611725/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200179449-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-OCT-2001.
                                                                                                                                                                                                                                                                                                              AAU30825;
                                                                                                                                        RESULT 15
AAU 30825
AAU 30825
ID AAU 30
XX
AC AAU 30
XX
DT 18-DE
XX
DE NOVE.
X
                                    g
```

Search completed: September 3, 2003, 11:46:12 Job time : 49.5 secs

g

ò

ö

; 0

Indels

0

Page

us-10-087-464-4.rag

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

September 3, 2003, 11:24:37 ; Search time 48.5 Seconds
(without alignments)
65.454 Million cell updates/sec Run on:

US-10-087-464-4

112 1 DRILLLFKPPKYHPDVPYVK 20 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1107863 seqs, 158726573 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries

Post-processing: Minimum Match 0%

A_Geneseq_19Jun03:* Database :

9.DAT:* /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*/SIDSI/gcgdata/geneseqp/geneseqp-embl/AA1983.DAT:*/SIDSI/gcgdata/geneseqp/geneseqp-embl/AA1984.DAT:*/SIDSI/gcgdata/geneseqp/geneseqp-embl/AA1986.DAT:*/SIDSI/gcgdata/geneseqp/geneseqp-embl/AA1986.DAT:*/SIDSI/gcgdata/geneseqp/geneseqp-embl/AA1986.DAT:*/SIDSI/gcgdata/geneseqp/geneseqp-embl/AA1986.DAT:*/SIDSI/gcgdata/geneseqp/geneseqp-embl/AA1988.DAT:*/SIDSI/geneseqp/geneseqp-embl/AA1988.DAT:*/SIDSI/g

.DAT:* /SIDS/19cgdata/geneseq/geneseqp-emb1/AA1989.DAT:
/SIDS/19cgdata/geneseq/geneseqp-emb1/AA1990.DAT:
/SIDS/19cgdata/geneseq/geneseqp-emb1/AA1990.DAT:
/SIDS/19cgdata/geneseq/geneseqp-emb1/AA1991.DAT:
/SIDS/19cgdata/geneseq/geneseqp-emb1/AA1993.DAT:
/SIDS/19cgdata/geneseq/geneseqp-emb1/AA1993.DAT:
/SIDS/19cgdata/geneseq/geneseqp-emb1/AA1994.DAT:
/SIDS/19cgdata/geneseq/geneseqp-emb1/AA1995.DAT:
/SIDS/19cgdata/geneseq/geneseqp-emb1/AA1995.DAT:
/SIDS/19cgdata/geneseq/geneseqp-emb1/AA1995.DAT:
/SIDS/19cgdata/geneseq/geneseqp-emb1/AA1995.DAT:
/SIDS/19cgdata/geneseq/geneseqp-emb1/AA1997.DAT:

/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998 /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /SIDS1/gcgdata/geneseg/genesegp-emb1/AA2000.DAT:*/SIDS1/gcgdata/geneseg/genesegp-emb1/AA2001.DAT:*/SIDS1/gcgdata/geneseg/genesegp-emb1/AA2002.DAT:*/SIDS1/gcgdata/geneseg/genesegp-emb1/AA2002.DAT:*/SIDS1/gcgdata/geneseg/genesegp-emb1/AA2003.DAT:*

			Description	Human Band 3 pepti	Human Band 3 prote	Exofacial region l	Human band 3 prote	Human erythrocyte	A. tigrinum AE1 pr	Human erythrocyte	Human Band 3 prote	Human Band 3 prote
CHTACHIOC			ΙD	AAE29342	AAE29350	AAW01095	AAB74886	AAR15355	AAW90263	AAB46914	AAE29343	AAE29344
			DB	23	23	17	22	12	20	22	23	23
			Length	20	51	58	58	911	911	911	911	911
	æ	Query	ore Match Length DB I	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
			Score	112	112	112	112	112	112	112	112	112
		Result	No.	П	7	m	4	ι.	9	7	80	6

Novel human secret Aged band 3 peptid Anjon transporter Band 3 protein loo A tigrinum AE2 pr A tigrinum AE3 pr A tigrinum AE3 pr A tigrinum AE3 pr Human liver peptid Peptide #1658 enco Protein #1559 enco Human brain expres Human brain expres Human brain expres Peptide #1539 enco Peptide #1539 enco Peptide #1539 enco Peptide #1579 enco Prosophila Na+ dri Drosophila Na+ dri Drosophila Na+ dri Drosophila Ma+ dri Drosophila Ma+ dri Drosophila melanog Drosophila melanog Larval viability a Drosophila melanog Larval viability a Drosophila melanog Larval viability a Drosophila Ma+ dri Drosophila melanog Larval viability a Drosophila Ma+ dri Drosophila melanog Larval viability a Drosophila Ma+ dri Drosophila melanog Larval viability a Drosophila Na+ dri Drosophila Ma+ dri Drosophila melanog Larval viability a Drosophila Na+ dri Drosophila Ma+ dri	bone polyp suppr human suppr suppr adipo
AAU30825 AAW18595 AAW18595 AAW18595 AAW18592 AAW90262 AAW90262 AAW90261 AAW90260 AAW90260 AAW90260 AAW31559 AAW5159 AAW5159 AAW77616	AAMUU / 59 ABP 69662 ABP 7586 ABP 60995 ABP 55448 AAW 18606
222222222222222222222222222222222222222	23 23 23 23 23 23
962 1140 1140 11740 1030 1030 1035 56 56 56 56 56 56 56 56 56 56 56 57 77 77 77 77 77 77 77 77 77 77 77 77	348 440 440 440 310
112 889 987 799 622 662 662 662 662 662 662 662 663 663	
110 1110 1110 1110 1110 1110 1110 1110	2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

AAE29342 standard; peptide; 20 AA. Human Band 3 peptide, B36A. (first entry) 27-JAN-2003 AAE29342; RESULT 1

Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine; protozoacide; gene therapy.

Homo sapiens.

WO200270542-A2.

12-SEP-2002.

01-MAR-2002; 2002WO-US06415.

02-MAR-2001; 2001US-272930P.

(SELI-) ST ELIZABETH'S MEDICAL CENT INC

Chishti AH, Oh SS, Liu D, Goel V;

WPI; 2002-759814/82.

New isolated Band 3 polypeptide which selectively binds to merozite surface protein-1, useful for the prevention and treatment of malarial infection

```
The invention relates to an isolated Band 3 polypeptide that comprises any of 4 20 residue amino acid sequences, or their fragments that bind to an MSP-1 polypeptide or a polypeptide with any of 8 291-131 base pair sequences. The methods and compositions of the present invention are useful for the prevention and treatment of malarial infection. The present invention, develops new and more improved methods based upon inhibiting the particular interactions between the malarial parasite and a cognate molecule present in the host and subsequently minimising therapeutic approaches. The invention is useful in gene therapy. The present invention also provides a vaccine for malaria. The present invention also provides a vaccine for malaria. The present
                                Page 84; 163pp; English
                                                                                                                                                                                                                                                                                                                                                                                         20 AA;
                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                  Claim 1;
```

Score 112; DB 23; Pred. No. 6.6e-10; 1 DRILLLFKPPKYHPDVPYVK 20 ó 100.0%; 100.0%; Query Match
Best Local Similarity 100.
Matches 20; Conservative ò

AAE29350 standard; peptide; 51 AA. RESULT

셤

AAE29350;

(first entry) 27-JAN-2003

Human Band 3 protein ectoplasmic domain 6.

Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine; protozoacide; gene therapy

Homo sapiens

WO200270542-A2.

12-SEP-2002.

01-MAR-2002; 2002WO-US06415.

02-MAR-2001; 2001US-272930P

(SELI-) ST ELIZABETH'S MEDICAL CENT INC.

Goel V; Liu D, Chishti AH, Oh SS,

WPI; 2002-759814/82

New isolated Band 3 polypeptide which selectively binds to merozite surface protein-1, useful for the prevention and treatment of malarial infection

Example; Page 58; 163pp; English.

The invention relates to an isolated Band 3 polypeptide that comprises any of 4 20 residue amino acid sequences, or their fragments that bind to an MSP-1 polypeptide or a polypeptide with any of 8 291-131 base pair sequences. The methods and compositions of the present invention are useful for the prevention and treatment of malarial infection. The present invention, develops new and more improved methods based upon inhibiting the particular interactions between the malarial parasite and harmful side effects and drug resistance that may be due to non specific therapeutic approaches. The invention is useful in gene therapy. The present invention also provides a vaccine for malaria. The present

```
Gaps
                                                                        ;
0
                                                 Length 51;
sequence is human Band 3 protein ectoplasmic domain 6.
                                             Score 112; DB 23;
Pred. No. 1.8e-09;
Mismatches 0;
                                                                                                            1 DRILLLEKPPKYHPDVPYVK 20
                                                                        ö
                                                100.0%;
100.0%;
                                               Query Match 100.0
Best Local Similarity 100.0
Matches 20, Conservative
                        51 AA;
                          Seguence
                                                                                                 ò
                                                                                                                       g
```

ö

RESULT 3 AAW01095

Ā AAW01095 standard; peptide; 58

AAW01095;

08-MAY-1997

ö

Gaps

ó

Mismatches

Length 20; Indels

(first entry)

Anion transporter band 3 protein; endothelial adhesion; red blood cell; cytoplasmic domain; erythrocyte; exofacial loop; epitope; antibody; mammal; plasmodium falciparum infection; sickle cell disease; diabetes; band 3; thalassaemia; anaemia; therapy.

Exofacial region loop 7 of band 3 protein (residues 800-857).

Synthetic.

WO9629086-A1.

26-SEP-1996

96WO-US03180. 07-MAR-1996;

(REGC) UNIV CALIFORNIA

Shohet SB, Thevenin BJ; Crandall IE, Sherman IW,

WPI; 1996-442944/44.

Peptide(s) with amino acid motifs in band 3 - used for reducing the adhesiveness of red blood cells for treating malaria, sickle cell disease, thalassemia or diabetes.

Example 2; Page 20; 48pp; English.

AAW01053-W01095 represent peptides isolated from (or based on) regions of the anion transporter band 3 protein. The band 3 protein is present in a million copies per red blood cell, in the form of monomers, dimers, or tetramers. Band 3 protein has two distinct domains, a 43 kD cortein because the form of monomers, dimers, we ater-soluble cytoplasmic domain, and a 55 kD membrane spanning domain. In an number of otherwise-unrelated conditions (such as malaria, and diabetes), there are modifications in band 3, such that there is clustering and a change in the conformation of the protein. Due to this change in protein conformation of the protein. Due to this change in protein conformation (and by the exposure of cryptic adhesive sites), the normally non-adherent erythrocyte becomes a cell with enhanced endothelial adhesiveness. These sequences were found in the putative exofacial loops of band 3, and are epitopes for antibody the adhesiveness of the red blood cells. The peptides can be used for reducing the adhesiveness of red blood cells. The peptides can be used for reducing the adhesiveness of red blood cells in a mammalian protein characterised by a condition selected from Plasmodium falciparum infection, sickle cell disease, thalassaemia and diabetes

58 AA; Sequence

Gaps ő Length 58; Indels 100.0%; Score 112; DB 17; ilarity 100.0%; Pred. No. 2.1e-09; Conservative 0; Mismatches 0; Local Similarity nes 20; Conserv Query Match Best Loca Matches

ó

 \sim

ò 셤

```
Synthetic senescent cell antigen and peptide(s) - used to detect antibodies to SCA, study cellular ageing and auto-immune mechanisms, separate anions and treat auto-immune disease
                                                                                                                                                                                                   Human erythrocyte membrane anion-transport protein (band 3).
                                                                                                                                                                                                                                       Senescent cell peptide; ANION 1; COOH; auto immune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (RESE ) RESEARCH CORP TECHNOLOGIES INC.
                                            AAR15355 standard; Protein; 911 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 1; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marchalonis JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1991-369184/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAQ15172.
                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                 24-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-MAY-1990;
                                                                                                                               25-MAR-2003
08-MAR-1992
                                                                                                                                                                                                                                                                                                                              WO9118013-A.
                                                                                                                                                                                                                                                                                                                                                                         28-NOV-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Кау МВМ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                         AAR15355;
    RESULT 5
AAR15355
                                                                                                                                                        The present invention describes a method for enhancing thrombolysis in a mammal. The method comprises the administration to the mammal an amount of an inhibitor (I) of protein band 3-ligand interaction

Sufficient to enhance thrombolysis. (I) has thrombolytic activity.

The method is useful for enhancing thrombolysis in a mammal. (I) is useful for enhancing fibrinolytic or thrombolytic activity, in the management of acute myocardial infarction, for Ilysis of intracoronary thrombi, for improvement of ventricular function, for reduction of congestive heart failure, for reduction of mortality, for the lysis of pulmonary emboli blocking blood flow to one or more lobes of the lung, for the lysis of acute arterial thrombosis and embolism, for the lysis of thrombosis in deep veins or in cerebral sinuses, to reopen i.v. catheters obstructed by clotted blood or fibrin, to prevent clotting in blood samples drawn from patients for clinical testing and to prevent the recurrence of trom patients for clinical testing and to prevent the recurrence of trom patients for clinical testing and to prevent the recurrence of trombosis in patients by prophylactic administration. The present sequence represents a human band 3 protein predicted exofacial region invention.
                                                                                                                                                                                                                                                                                                                        Anti-Plasmodium falciparum; interaction inhibitor; band 3 protein; thrombolysis; thrombolytic; fibrinolytic; acute myocardial infarction; lysis; ventricular function; congestive heart failure; mortality; acute arterial thrombosis; embolism; thrombosis; cerebral sinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enhancing thrombolysis in mammals comprises administering an inhibitor of protein band 3-ligand interaction
                                                                                                                                                                                                                                                                                 Human band 3 protein predicted exofacial region loop 7 SEQ ID NO:43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 100.0%; Score 112; DB 22;
1 Similarity 100.0%; Pred. No. 2.1e-09;
20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Von Andrian U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Column 7; 23pp; English
                                                                                                                                                    AAB74886 standard; peptide; 58 AA
                      8 DRILLERPPKYHPDVPYVK 27
DRILLLFKPPKYHPDVPYVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0985499.
                                                                                                                                                                                                                                    19-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (REGC ) UNIV CALIFORNIA. (BLOO-) CENT BLOOD RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shohet SB, Sherman I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-307101/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US6191103-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0-FEB-2001
                                                                                                                                                                                              AAB74886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                             AAB74886
                                                                                                           RESULT
```

91WO-US03557.

(first entry)

(updated)

```
The amino acid sequence is that of the human erythrocyte anion-transport protein (band 3). Amino acids 538-554 (ANION 1) or 812-827 (COOH) code for a peptide which is immuno-reactive with antibodies to senescent cell antigen (SCA). The antigen and peptides can be used in any method or technique involving or requiring the inhibition of the binding of senescent cell 1gG to senescent cells in vitro or in vivo. The prods. can be used in to examine various physiological, biochemical, and immunological mechanisms in humans and other animals, such as those relating to cellular ageing, degeneration, and life span; removal of senescent cells; anion transport across cellular membranes; disease mechanisms where increased senescent cell 1gG may play a role, such as haemolytic anaemia, sickle cell anaemia, and idiopathic thrombocytopenia purpura; other autoimmune disease mechanisms, such as haemolytic anaemia, sickle cell anaemia, and idiopathic chrombocytopenia purpura; other autoimmune disease mechanisms, such as rheumatoid arthritis and systemic lupus erythematosus; and other diseases such as those involved in malaria and cancer. More specifically, the prods are useful in cosmetic and pharmaceutical comparations, diagnostic kits, and methods for detecting or measuring compassuring and chromans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Abs to SCA, studying cellular ageing and autoimmune mechanisms, spearating anions from a gas or liquid, or diagnosis and treatment of certain diseases (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , 4e-08;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 112; DE;
; Pred. No. 4e-(
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW90263 standard; peptide; 911 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   807 DRILLLEKPPKYHPDVPYVK 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DRILLLEKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 20; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW90263
ID AAW9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

ö

Gaps

ö

Indels

1 DRILLLFKPPKYHPDVPYVK 20

ò g

```
This sequence represents the anion exchange protein AEI which is used in a method resulting in the isolation of a novel salamander sodium bicarbonate transporter (NBC). NBC proteins and nucleic acid sequences may be used to treat pathological processes including water retention, increased blood pressure, chronic respiratory and metabolic acidosis, inflammation, cell proliferation, cancer, sperm activation/inactivation, hydroencephaly, epilepsy, glaucoma and collitis. Members of the NBC family of proteins can be used (1) as a target to identify agents that block or stimulate NBC mediated pH regulation, (ii) as a target or bait to identify and isolate binding partners that bind NBC, (iii) in methods to identify agents that block or stimulate eactivity of an NBC protein, and (iv) as a target to assay for NBC-mediated activity, Anti-NBC antibodies are also useful as modulators of NBC activity, useful in the immunoassays
                                                                                                                        NBC; sodium bicarbonate transporter family; pH regulation; immunoassay; treatment; water retention; blood pressure; acidosis; inflammation; cell proliferation; cancer; sperm activation; inactivation; epilepsy; hydroencephaly; glaucoma; colitis; salammander; ABI; anion exchange.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detecting NBC expression/activity and for purifying an NBC protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid molecules encoding proteins of the Sodium Bicarbonate Corransporter (NBC) family - useful for identifying agents that agonise or antagonise NBC activity and treating disorders mediated by NBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                Aalkjaer C, Bevensee MO, Biemesderfer D, Boron WF;
Choi I, Davis BA, Grichtchenko II, Romero MF, Schmitt BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 112; DB 20; Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human erythrocyte band 3 anion transporter protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 4e-08;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB46914 standard; protein; 911 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Fig 5; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DRILLLFKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                           98WO-US10297.
                                                                                                                                                                                                                                                                                                                                                             97US-0047131
                                                    27-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
                                                                                       A. tigrinum AE1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-059743/05
                                                                                                                                                                                                                   Ambystoma tigrinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                (UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                   W09853067-A1
                                                                                                                                                                                                                                                                                                                         20-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                             20-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAY-2001
                                                                                                                                                                                                                                                                                      26-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sussman CR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB46914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
XEXEXEX
```

```
physiological effect of a composition comprising hemoglobin which involves obtaining electron paramagnetic resonance (EPR) or UV spectra iron-nitrosyl hemoglobin derivatives formed by incubation of limiting nitric oxide (NO) with hemoglobin and determining if the composition shows non-cooperativity or cooperativity in binding of NO to the memoglobin. The products of the invention have antianemic; antibacterial; immunosuppressive; vasotropic; antiinflammatory; antiasthmatic; respiratory; antiarthritic and cerebroprotective activity. The products of the invention are used to produce methods of therapy for medical disorders characterized by red blood cell membrane defects and for a variety of hypercoagulable and vasculopathic states, particularly for patients with septic shock who develop myocardial depression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pancreatitis and progressive respiratory failure, patients with septicemia as a complication of urinary tract infection and patients with stochmia, patients in a sickle cell crisis and for treating inflammatory conditions such as arthritis, asthma, cerebritis, bronchitis and vasculitis. The methods are also used for preserving red blood cells
Erythrocyte band 3 anion transporter protein; human, hypercoagulation; iron-nitrosyl hemoglobin; electron paramagnetic resonance; UV spectra; EPR; nitric oxide; antianemic; antibacterial; immunosuppressive; vasotropic; antiinflammatory; antiasthmatic; respiratory; antiarthritic; cerebroprotective; red blood cell membrane defect; vasculopathy; septic shock mycoardial depression; pancreattis; sickle cell crisis; urinary tract infection; progressive respiratory failure; septicemia; ischemia; arthritis; asthma; cerebritis; bronchitis; vasculitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel method for determining the predominant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Determining predominant physiological effect of composition comprising hemoglobin used to produce methods of therapy for medical disorders by using EPR or UV spectra of iron nitrosyl hemoglobin derivatives -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 112; DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 4e-08;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE29343 standard; Protein; 911 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 11; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DRILLLFKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                02-AUG-2000; 2000WO-US21101.
                                                                                                                                                                                                                                                                                                                                                                                                                                        (RERE-) RES & DEV INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Band 3 protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GOW AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-183002/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                    (UYDU-) UNIV DUKE.
                                                                                                                                                                                                                                           WO200109616-A2.
                                                                                                                                                                                                                                                                                                                                                                        02-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stamler JS,
                                                                                                                                                                                                                                                                                      38-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE29343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

(SELI-) ST ELIZABETH'S MEDICAL CENT INC.

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated Band 3 polypeptide that comprises any of 4 20 residue amino acid sequences, or their fragments that bind to an MSPO-1 polypeptide or a polypeptide with any of 8 291-131 base pair sequences. The methods and compositions of the present invention are useful for the prevention and treatment of malarial infection. The present invention, develops new and more improved methods based upon inhibiting the particular interactions between the malarial parasite and a cognate molecule present in the host and subsequently minimising thermpeutic approaches. The invention is useful in gene therapy. The present invention also provides a vaccine for malaria. The present sequence is human Band 3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine; protozoacide; gene therapy.
Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine;
protozoacide; gene therapy.
                                                                                                                                                                                                                                                                                                 New isolated Band 3 polypeptide which selectively binds to merozite surface protein-1, useful for the prevention and treatment of malarial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 112; DB 23; Length 911; 100.0%; Pred. No. 4e-08; O; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 102-105; 163pp; English.
                                                                                                                                                                                              (SELI-) ST ELIZABETH'S MEDICAL CENT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE29344 standard; Protein; 911 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DRILLLFKPPKYHPDVPYVK 20
                                                                                                                                                                02-MAR-2001; 2001US-272930P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002; 2002WO-US06415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAR-2001; 2001US-272930P
                                                                                                                                  01-MAR-2002; 2002WO-US06415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Band 3 protein #2.
                                                                                                                                                                                                                          oh ss,
                                                                                                                                                                                                                                                      WPI; 2002-759814/82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        911 AA;
                                                                                                                                                                                                                                                                       N-PSDB; AAD46978
                                                                         WO200270542-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-JAN-2003
                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                          Chishti AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-SEP-2002.
                                                                                                      12-SEP-2002
                                                                                                                                                                                                                                                                                                                                  infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE29344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

```
inhibiting the particular interactions between the malarial parasite and a cognate molecule present in the host and subsequently minimising harmful side effects and drug resistance that may be due to non-specific therapeutic approaches. The invention is useful in gene therapy. The present invention also provides a vaccine for malaria. The present sequence is human Band 3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
                                                                                                                                                                                                                                                                                        any of 4 20 residue amino acid sequences, or their fragments that bind to an MSP-1 polypeptide or a polypeptide with any of 8 291-1331 base pair sequences. The methods and compositions of the present invention are useful for the prevention and treatment of malarial infection. The present invention, develops new and more improved methods based upon
                                                                                                                                            New isolated Band 3 polypeptide which selectively binds to merozite surface protein-1, useful for the prevention and treatment of malarial
                                                                                                                                                                                                                                                                      The invention relates to an isolated Band 3 polypeptide that comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 112; DB 23;
100.0%; Pred. No. 4e-08;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 112,
Pred. No. 4e-08;
                                                                                                                                                                                                                             Disclosure; Page 107-110; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human secreted protein #1316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU30825 standard; Protein; 962 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; Page 354; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DRILLLFKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-APR-2001; 2001WO-US08656.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-APR-2000; 2000US-0552929.
26-JAN-2001; 2001US-0770160.
                                     Liu D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-611725/70.
                                                                              WPI; 2002-759814/82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C,
                                                                                                  N-PSDB; AAD46979
                                       o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200179449-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU30825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU30825
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are useful for identifying agents (agonists and antaponists) that bind to them. Cells capressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptides vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU2510-AAU3304 represent the amino acid sequences of novel human secreted proteins of the invention. invention relates to novel human secreted polypeptides. The 962 AA; Sequence

Length 962; Indels 100.0%; Score 112; DB 22; 100.0%; Pred. No. 4.2e-08; 0; Mismatches 1 DRILLLFKPPKYHPDVPYVK 20 Best_Local Similarity 100. Matches '20; Conservative Query Match 셤 ŏ

ö

Gaps

ó

AAW18594

AAW18594 standard; peptide; 16 AA

AAW18594;

(first entry) 04-MAR-1998 Aged band 3 peptide (residues 812-827) epitope I.

Band 3 protein; antibody; aging antigenic site; Alzheimer's disease; phosphorylation; detection; epitope. THE STATE OF THE S

Homo sapiens

WO9726537-A1

24-JUL-1997.

96WO-US20465 13-DEC-1996; (RESE) RESEARCH CORP TECHNOLOGIES INC.

19-JAN-1996;

WPI; 1997-385478/35.

Detecting Alzheimer's disease using antibody that recognises aged band 3 protein in tissues - or from reduced degree of band 3 protein phosphorylation, can be applied to blood or brain samples

Claim 6; Page 11; 45pp; English.

This is an aging antigenic band 3 peptide (residues 812-827) to which a specific antibody can bind to. Band 3 is a ubiquitous anion-exchange protein and ages as cells and tissues age. Antibodies have been developed against this aged band 3. These antibodies bind to distinct regions of band 3 in old cells (aging antigenic sites) but not middle aged or young cells. This can be used for detecting Alzheimer's disease. A tissue sample containing band 3 from a patient suspected of having Alzheimer's disease is treated with an antibody that can differentiate between the Alzheimer's (aged) and normal band 3, under complex-forming conditions

in the suspect sample indicates Alzheimer's disease.

This is an aging antigenic band 3 peptide (residues 812-830) to which a specific antibody can bind to. Band 3 is a ubiquitous anion-exchange protein and ages as cells and tissues age. Antibodies have been developed against this aged band 3. These antibodies bind to distinct regions of band 3 in old cells (aging antigenic sites) but not middle aged or young cells. This can be used for detecting Alzheimer's disease. A tissue cample containing band 3 from a patient suspected of having Alzheimer's disease is treated with an antibody that can differentiate between the Alzheimer's (aged) and normal band 3, under complex-forming conditions and detecting any complex formed. A tissue containing band 3 from a healthy control is treated in a similar manner and the amounts of complex formed are compared. A significantly greater formation of complex in the suspect sample as compared with that of the control is indicative of Alzheimer's disease can also be detected by comparing the degrees of phosphorylation of band 3 or its degradation products in suspect and control samples. A significant decrease in phosphorylation ö and detecting any complex formed. A tissue containing band 3 from a healthy control is treated in a similar manner and the amounts of compl formed are compared. A significantly greater formation of complex in the suspect sample as compared with that of the control is indicative of Alzheimer's disease. The diseases can also be detected by comparing the degrees of phosphorylation of band 3 or its degradation products in suspect and control samples. A significant decrease in phosphorylation in the suspect sample indicates Alzheimer's disease. Detecting Alzheimer's disease using antibody that recognises aged band 3 protein in tissues – or from reduced degree of band 3 protein phosphorylation, can be applied to blood or brain samples Band 3 protein; antibody; aging antigenic site; Alzheimer's disease; phosphorylation; detection; epitope. ö Length 16; Indels Aged band 3 peptide (residues 812-830) epitope II. DB 18; L Pred. No. 1.4 Mismatches 79.5%; Score 89; (RESE) RESEARCH CORP TECHNOLOGIES INC. AAW18595 standard; peptide; 19 AA. 79.008; FI Claim 7; Page 10; 45pp; English. 96WO-US20465. 96US-0010250 1 LFKPPKYHPDVPYVK 15 6 LFKPPKYHPDVPYVK 20 (first entry) Best_Local Similarity 100. Matches 15; Conservative WPI; 1997-385478/35. 16 AA; Homo sapiens WO9726537-A1 13-DEC-1996; 19-JAN-1996; 04-MAR-1998 Sequence AAW18595; Query Match AAW18595 888888888888 g δ

1 KPPKYHPDVPYVK 13

S

RESULT

δ g

```
AAB74852 standard; peptide; 14 AA.
                                                                                                AAB74852
                     g
                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW01053-W01095 represent peptides isolated from (or based on) regions of the anion transporter band 3 protein. The band 3 protein is present in a million copies per red blood cell, in the form of monomers, dimers, or tetramers. Band 3 protein has two distinct domains, a 43 kD water-soluble cytoplasmic domain, and a 55 kD membrane spanning domain. In an number of otherwise-unrelated conditions (such as malaria, and diabetes), there are modifications in band 3, such that there is clustering and a change in the conformation of the protein. Due to this change in protein conformation (and by the exposure of cryptic adhesive sites), the normally non-adherent erythrocyte becomes a cell with cananced endothelial adhesiveness. These sequences were found in the putative exofacial loops of band 3, and are epitopes for antibody binding. These sequences compete with the altered band 3 protein, and thereby block the adhesiveness of the red blood cells. The peptides can be used for reducing the adhesiveness of red blood cells in a mammalian patient characterised by a condition selected from plasmodium falciparum infection, sickle cell disease, thalassaemia and diabetes.
                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                            Anion transporter band 3 protein; endothelial adhesion; red blood cell; cytoplasmic domain; errythrocyte; exofacial loop; epitope; antibody; mammal; plasmodium falciparum infection; sickle cell disease; diabetes; band 3; thalassaemia; anaemia; therapy.
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide(s) with amino acid motifs in band 3 - used for reducing the adhesiveness of red blood cells for treating malaria, sickle cell
                                                                            ;
0
                               Score 89; DB 18; Length 19;
Pred. No. 1.7e-06;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thevenin BJ;
                                                                                                                                                                                                                                                                                                                                                          Anion transporter band 3 protein residues 814-827,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shohet SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 12; 48pp; English.
                                                                                                                                                                                                                                             AAW01080 standard; peptide; 14 AA.
                   79.5%; Scu-
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease, thalassemia or diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96WO-US03180.
                                                                                                                                 1 LEKPPKYHPDVPYVK 15
                                                                                                             6 LFKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-0405647
                                                                                                                                                                                                                                                                                                                     08-MAY-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sherman IW,
                                                                        15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-442944/44.
                                   Query Match
Best Local Similarity
19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Crandall IE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9629086-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L7-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
 Sequence
                                                                                                                                                                                                                                                                                AAW01080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                        Matches
                                                                                                                                                                                                                           AAW01080
```

```
The present invention describes a method for enhancing thrombolysis in a mammal. The method comprises the administration to the mammal and amount of an inhibitor (I) of protein band 3-ligand interaction

sufficient to enhance thrombolysis. (I) has thrombolytic activity.

The method is useful for enhancing thrombolysis in a mammal. (I) is useful for enhancing fibrinolytic or thrombolytic activity, in the management of acute myocardial infarction, for lysis of intracoronary thrombi, for improvement of ventricular function, for reduction of congestive heart failure, for reduction of mortality, for the lysis of pulmonary emboli blocking blood flow to one or more lobes of the lung, for the lysis of acute arterial thrombosis and embolism, for the lysis of thrombosis in deep veins or in cerebral sinuses, to reopen i.v.

catheters obstructed by clotted blood or fibrin, to prevent clot formathon of lysing clots, to prevent clotting in blood samples drawn from patients for clinical testing and to prevent the recurrence of thrombosis in patients by prophylactic administration. The present sequence represents a band 3 protein loop 3 related peptide, which is given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                           infarction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enhancing thrombolysis in mammals comprises administering an inhibitor of protein band 3-ligand interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                    Anti-Plasmodium falciparum; interaction inhibitor; band 3 protein; thrombolysis; thrombolytic; fibrinolytic; acute myocardial infarct lysis; ventricular function; congestive heart failure; mortality; acute arterial thrombosis; embolism; thrombosis; cerebral sinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                       Band 3 protein loop 3 related peptide SEQ ID NO:9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22; Lot 3.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.5%; Score 79; DB 100.0%; Pred. No. 3.7 iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Von Andrian U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Column 8; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-0985499.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-0985499
                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 70.5 Best Local Similarity 100. Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 KPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KPPKYHPDVPYVK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (REGC ) UNIV CALIFORNIA. (BLOO-) CENT BLOOD RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shohet SB, Sherman I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-307101/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                               US6191103-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-DEC-1997;
                                                                   19-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
AAB74852;
```

Query Match 70.5 Best Local Similarity 100. Matches 13; Conservative

RESULT 15 AAW90262

ö

Gaps

; 0

0; Indels

70.5%; Score 79; DB 17; Length 14; 100.0%; Pred. No. 3.7e-05;

```
In Sequence represents the annual external mass mixes, a water as method resulting in the isolation of a novel salamander sodium bicarbonate transporter (NBC). NBC proteins and nucleic acid sequences may be used to treat pathological processes including water retention, increased blood pressure, chronic respiratory and metabolic acidosis, inflammation, cell proliferation, cancer, sperm activation/inactivation, hydroencephaly, epilepsy, glaucoma and colitis. Members of the NBC family of proteins can be used (i) as a target to identify agents that block or stimulate NBC mediated pH regulation, (ii) as a target or bait to identify agents that block or stimulate activity of an NBC, (iii) in methods to identify agents that block or stimulate activity of an NBC protein, and (iv) as a target to assay for NBC-mediated activity. Anti-NBC antibodies are also useful as modulators of NBC activity, useful in the immunoassays for detecting NBC expression/activity and for purifying an NBC protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents the anion exchange protein AE2 which is used in
                                                                                                                                                       NBC; sodium bicarbonate transporter family; pH regulation; immunoassay; treatment; water retention; blood pressure; acidosis; inflammation; cell proliferation; cancer; sperm activation; inactivation; epilepsy; hydroencephaly; glaucoma; colitis; salamander; AE2; anion exchange.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid molecules encoding proteins of the Sodium Bicarbonate Cotransporter (NBC) family - useful for identifying agents that agonise or antagonise NBC activity and treating disorders mediated by NBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C, Bevensee MO, Biemesderfer D, Boron WF;
Davis BA, Grichtchenko II, Romero MF, Schmitt BM;
AAW90262 standard; peptide; 1240 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Fig 5; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                98WO-US10297
                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0047131
                                                                          (first entry)
                                                                                                                  A. tigrinum AE2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-059743/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1240 AA;
                                                                                                                                                                                                                                                                Ambystoma tigrinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                   WO9853067-A1.
                                                                                                                                                                                                                                                                                                                                                                                20-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                        20-MAY-1997;
                                                                          27-APR-1999
                                                                                                                                                                                                                                                                                                                                          26-NOV-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aalkjaer C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sussman CR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence
                                   AAW90262;
```

ö Gaps ö 66.1%; Score 74; DB 20; Length 1240; 65.0%; Pred. No. 0.026; 1.ive 3; Mismatches 4; Indels C Query Match 66.1 Best Local Similarity 65.0 Matches 13; Conservative

1 DRILLLFKPPKYHPDVPYVK 20

:|: || |||:||| ||| 1136 ERLHLLLMPPKHHPDVTYVK 1155

g

Search completed: September 3, 2003, 11:46:13 Job time: 49.5 secs

us-10-087-464-1.rsp

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

September 3, 2003, 11:25:42 ; Search time 9.25 Seconds
(without alignments)
101.679 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-087-464-1 104 1 GMPWLSATTVRSVTHANALT 20

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		sapien	norv	culu	gall	nchu	norv	culu	agus	pien	culu	norv	pien	agus	orce	agus	teri	norv	pien	bact	norv	culu	teri	pien	es 1	teri	pien	acch	chia	chia	iril	abdi	cter	scrofa
	ption	homo	rattus norv	mus musculu	gallus gal		rattus norv	mus musculu	oryctolagus		_	rattus norv		-	cavia porce	_	mycobacteri	_	homo sapien	methanobact	rattus norv	_	mycobacteri	_	hylobates l	mycobacteri			-	-	rhodospiri	•	caulobacter	sns
	Description	P02730	P23562	P04919	P15575	P32847	P23347	P13808	P48746	P04920	P16283	P23348	P48751	018917	09z0s8	Q9gky1	032962	08k4v2	096491	027083	P51556	088673	008447	Q8nbs3	095708	010380	P00749	Q9c104	P32710	P14176	P23134	003603	. 09abz8	P04185
SUMMARIES		IMAN	Ħ	OUSE	IICK	CMX	턴	USE	BIT	IMAN	USE	Ħ	IMAN	BIT	CAVPO	BIT	CLE	Ţ	IMAN	TTH	Ţ	USE	CIU	IMAN	LLA	CIU	IMAN	HPO:	OLI	:0LI)RU	CAEEL	NUCR	9
SOM	ΩI	B3AT_HUMA	B3AT_RAT	B3AT_MOUSE	B3AT_CHICK	B3AT_ONCMY	B3A2_RAT	B3A2_MOUSE	B3A2_RABIT	B3A2_HUMAN	B3A3_MOUSE	B3A3_RAT	B3A3_HUMAN	B3A3_RABIT	B3A2_CP	B3A4_RABIT	LIPA_MYCLE	B3A4_RAT	B3A4_HUMAN	COBK_METTH	KDGA_RAT	KDGA_MOUSE	C13A_MYCTU	SL11_HUMAN	NU3M_HYLLA	LIPA_MYCTU	UROK_HUMAN	YKT5_SCHPO	NRFE_ECOLI	PROW_ECOLI	CYB_RHORU	KDGL_C	HEM3_CAUCR	UROK_PIG
	DB	7	7	٦	7	7	٦	7	٦	٦	7	٦	Н	~	٦	П	П	П	7	٦	٦	7	7	-	-	Н	7	Т	-	٦	٦	-	-	-
	Query Match Length DB	911	927	929	922	918	1234	1237	1237	1241	1227	1227	1232	1233	1238	955	314	953	983	302	727	730	449	891	115	311	431	1076	552	354	405	827	322	442
ď	Query Match	100.0	100.0	100.0	96.2	ä	89.4	89.4	89.4	6	S.	'n	ď.	Ľ.	σ.	7	ė.	ė.		۳,	ω.		ς.	ς.	;	٠	1	;	40.9		40.4	0	39.4	39.4
	Score	104	104	104	100	95	93	93	93	93	88	88	88	83	83	49	48	48	48	45	45	45	44	44	43	43		4	42.5		42		41	41
	Result No.	П	7	e	4	2	9	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59	30	31	32	33

P11078 recvirus (t P20192 sus scrofa	P42703 mus musculu P12915 b genome po Q91zi0 mus musculu	Q9nyq7 homo sapien O88278 rattus norv	064319 rattus norv P51208 porphyra pu	P56938 rhodobacter P07519 hordeum vul	P15321 serratia ma
VM2_REOVD KDGA_PIG	LIFR_MOUSE POLG_BOVEV CLR3_MOUSE	CLR3_HUMAN CLR3_RAT	SC31_RAT YC56_PORPU	COXX_RHOSH CBP1_HORVU	HLYB_SERMA
1		٦٦			7
709	1092 2175 3301	3312 3313	683 263	284 499	557
4.4	39.4 39.4	4. 4.	ن بن	2.5	5.
39	39	39	38	38	38
41	4 41 41	4 4 4 1	40.5	40 40	40
34 35	36 38 38	39 40	41	43	45

ALIGNMENTS

~

Sep

"Sequential phosphorylation of protein band 3 by Syk and Lyn tyrosine kinases in intact human erythrocytes: identification of primary and secondary phosphorylation sites."; Blood 96:1550-1557(2000) Kawano Y., Okubo K., Tokunaga F., Miyata T., Iwanaga S., Hamasaki N.; "Localization of the pyridoxal phosphate binding site at the COOH-terminal region of erythrocyte band 3 protein."; J. Biol. Chem. 263:8232-8238(1988). conformation and a possible molecular mechanism for anion VARIANT HE 400-ALA--ALA-408 DEL, AND VARIANT MEMPHIS GLU-56.
MEDLINE-92107882; PubMed-1722314;
Jarolim P., Palek J., Amato D., Hassan K., Sapak P., Nurse G.T.,
Rubin H.L., Zhai S., Sahr K.E., Liu S.-C.;
"Deletion in erythrocyte band 3 gene in malaria-resistant Southeast
Asian ovalocytosis."; VARIANT HE 400-ALA--ALA-408 DEL.
MEDLINE-92167271; PubMed=1538405;
Schoffield A.E., Tanner M.J. A., Phinder J.C., Clough B., Bayley P.M., Nash G.B., Dluzewski A.R., Reardon D.M., Cox T.M., Wilson R.J.M., Okubo K., Hamasaki N., Hara K., Kageura M.;
"Palmitoylation of cysteine 69 from the COOH-terminal of band 3 protein in the human erythrocyte membrane. Acylation occurs in the middle of the consensus sequence of F-I-IICLAVL found in band 3 protein and G2 protein of Rift Valley fever virus.";
J. Biol. Chem. 266:16420-16424(1991). PHOSPHORYLATION OF TYR-8; TYR-21; TYR-359 AND TYR-904.
BENDALINE-20400020; Pubmed-10942405;
BENDALI A.M., Bordin L., Clari G., James P., Quadroni M., Baritono Pinna L.A., Donella-Deana A.; VARIANT HS ARG-127.

MEDLINE-92229950; PubMed=1378323;
Jarolin P., Palek J., Rubin H.L., Prchal J.T., Korsgren C.,
Cohen C.M.;

"Band 3 Tuscaloosa: Pro-327-->Arg substitution in the cytoplasmic
domain of erythrocyte band 3 protein associated with spherocytic
hemolytic anemia and partial deficiency of protein 4.2.";
Blood 80:523-529(1992). "Anion-proton cotransport through the human red blood cell band 3 protein. Role of glutamate 681."; J. Biol. Chem. 267:13964-13971(1992). MEDLINE=91329825; PubMed=1678289; Yannoukakos D., Vasseur C., Driancourt C., Blouquit Y., Delauney Wajcman H., Bursaux E.; "Human erythrocyte band 3 polymorphism (band 3 Memphis): Characterization of the structural modification (Lys 56-->Glu) by protein chemistry methods."; Blood 78:1117-1120(1991). "Basis of unique red cell membrane properties in hereditary Proc. Natl. Acad. Sci. U.S.A. 88:11022-11026(1991) ROLE OF GLU-681, AND SEQUENCE OF 665-688 MEDLINE-92332495, PubMed=1352774; Jennings M.L., Smith J.S.; SEQUENCE OF 834-911. MEDLINE=88228050; PubMed=3372523; MEDLINE-91358422; PubMed-1885574; MEDLINE-93343855; PubMed-8343110; Mol. Biol. 223:949-958(1992) lochem. J. 213:577-586(1983). PALMITOYLATION OF CYS-843. VARIANT MEMPHIS GLU-56. VARIANT HS LEU-868. ovalocytosis." Nash G.B., Dl Gratzer W.B.; sednence, 101

ы :

VARIANTS HS GLN-760; TRP-760; CYS-808 AND TRP-870.
MEDLINE-95134893; PubMed=7530501;
Jarolim P., Rubin H.L., Brabec V., Chrobak L., Zolotarev A.S.,
Alper S.L., Brugnara C., Wichterle H., Palek J.;
"Mutations of conserved arginines in the membrane domain of erythroid band 3 lead to a decrease in membrane-associated band 3 and to the phenotype of hereditary spherocytosis.";
Blood 85:634-640(1995). "Human erythrocyte protein 4.2 deficiency associated with hemolytic anemia and a homozygous 40 glutamic acid-->lysine substitution in the cytoplasmic domain of band 3 (band 3Montefiore)."; Blood 81:2155-2165(1993) VARIANTS HS SER-147 AND MET-488.
MEDLINE-97351102; PubMed-9207478;
Alloisio N., Texier P., Vallier A., Ribeiro M.L., Morle L., Bozon M.,
Bursaux E., Maillet P., Goncalves P., Tanner M.J., Tamagnini G., Bruce L.J., Kay M.M., Lawrence C., Tanner M.J.; "Band 3 HT, a human red-cell variant associated with acanthocytosis and increased anion transport, carries the mutation Pro-868-->Leu in the membrane domain of band 3."; Bruce L.J., Anstee D.J., Spring F.A., Tanner M.J.; "Band 3 Wemphis variant II. Altered stilbene disulfonate binding and the Diego (Dia) blood group antigen are associated with the human erythrocyte band 3 mutation Pro-854-->Leu."; J. Biol. Chem. 269:16155-16158(1994). VARIANT HS ASP-771.
MEDIJNE=96136073; PubMed=8547122;
Maillet P., Vallier A., Reinhart W.H., Wyss E.J., Ott P., Texier P.,
Ballouti F., Tanner M.J., Delaunay J., Allolsio N.;
"Band 3 Chur: a variant associated with band 3-deficient hereditary
spherocytosis and substitution in a highly conserved position of "Changes in the blood group Wright antigens are associated with a mutation at amino acid 658 in human erythrocyte band 3: a site of interaction between band 3 and glycophorin A under certain MEDLINE-96225450; PubMed-8640229;
Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,
Dornwell M., Herbers J., Kugler W., Oezcan R., Pekrun A.,
Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.,
"Ankyrin-1 mutations are a major cause of dominant and recessive "Characterization of 13 novel band 3 gene defects in hereditary spherocytosis with band 3 deficiency."; Blood 88:4366-4374(1996). Jarolim P., Murray J.L., Rubin H.L., Taylor W.M., Prchal J.T., Ballas S.K., Snyder L.M., Chrobak L., Melrose W.D., Brabec V., MEDLINE-93229758; PubMed-8471774; Rybicki A.C., Qiu J.J.H., Musto S., Rosen N.L., Nagel R.L., Schwartz R.S.; Bruce L.J., Ring S.M., Anstee D.J., Reid M.E., Wilkinson S., VARIANTS HS ASP-285; GLU-455; PRO-707; PRO-834 AND MET-837 MEDLINE-97099297; PubMed-8943874; VARIANTS HS LYS-40; CYS-518 AND MET-663 DEL VARIANT BLOOD GROUP DI(A)/MEMPHIS-II. MEDLINE-94266802; PubMed-8206915; Br. J. Haematol. 91:804-810(1995). VARIANT BLOOD GROUP WR(A). MEDLINE=95111140; PubMed=7812009; Biochem. J. 293:317-320(1993). hereditary spherocytosis."; Nat. Genet. 13:214-218(1996). [16]
VARIANT MONTEFIORE LYS-40 Blood 85:541-547(1995). transmembrane segment conditions. Tanner M.J Palek J

 \sim

```
Lipoprotein;
                                                                                                                          DOMAIN
TRANSMEM
                                                                                                                                                                                                                              SEQUENCE
                                                                                            RANSMEM
                                                                                                                TRANSMEM
                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                          VARSPLIC
                                                                       PRANSMEM
                                                                                                                                             TRANSMEM
                                                                                                                                                         TRANSMEM
                                                                                                                                                                  TRANSMEM
                                                                                                                                                                            TRANSMEM
                                RANSMEM
                                         RANSMEM
                                                   TRANSMEM
                                                              RANSMEM
             DOMAIN
                       DOMAIN
                                                                                  DOMAIN
                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                           P04919
                                                                                                                                                                                                                                                                                                                                            RESULT 3
B3AT_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                             (MEB3)
                                                                                                                                                                                                                                                                        Matches
   δ
                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                               ö
                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rođentia; Sciurognathi; Muridae; Murinae; Rattus.
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              AND APPEARS TO BE TETRAMERIC.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. IN THE
BASOLATERAL MEMBRANE OF INTERCALATED CELLS OF DISTAL TUBULES AND
                                                                                                                                                                                                                                                                    MEDLINE-89255254; PubMed-2722777;
Kudrycki K.E., Shull G.E.,
"Primary structure of the rat kidney band 3 anion exchange protein
                                                                                                                                                    28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Band 3 anion transport protein (Anion exchange protein 1) (AE 1).
                               ;
0
          Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGREAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;
                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: Kidney. SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=2;
           DB 1;
                              ö
         Score 104; DF
Pred. No. 4.36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=P23562-2; Sequence=VSP_000455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=Erythrocyte;
IsoId=P23562-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A33810; A33810.
HSSP; P02730; 1BTS.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                    deduced from a cDNA.";
J. Biol. Chem. 264:8185-8192(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; J04793; AAA40800.1; ALT_INIT
EMBL; L02943; AAA40801.1; -.
                                                            720 GMPWLSATTVRSVTHANALT 739
  100.0%; Scur
100.0%; Pre
0;
                                                  1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00955; HC03_cotransp; 1.
PRINTS; PR01231; HC03TRNSPORT.
                                                                                                                                            01-NOV-1991 (Rel. 20, Created)
                                                                                                                                                                                                                                               SEQUENCE OF 46-927 FROM N.A.
                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-45 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALTERNATIVE PRODUCTS:
                              Conservative
                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                              COLLECTING DUCTS
Query Match
Best Local Similarity .
20; Conserve
                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=Kidney;
                                                                                                                                                                                    SLC4A1 OR AE1.
                                                                                                                                                                                                                                                           TISSUE=Kidney;
                                                                                                                         B3AT_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         +
                                                                                                               B3AT_RAT
                                                                                                     RESULT
                                                  ŏ
                                                                    ద
```

```
Kopito R.R., Lodish H.F.; "Primary structure and transmembrane orientation of the murine anion exchange protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse),
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Band 3 anion transport protein (Anion exchange protein 1) (AE 1)
                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (PROBABLE). PALMITATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 927;
                                                                                                                                                                                                                       POTENTIAL. EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                         Missing (in isoform Kidney).
                                                                                                                                       POTENTIAL. EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PARTIAL SEQUENCE FROM N.A. MEDILINE-87250387; MEDILINE-87250387; Andersson M., Lodish H.F.; Structure and organization of the murine band 3 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUL-1987) to the EMBL/GenBank/DDBJ databases.
                   CYTOPLASMIC (POTENTIAL). MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                            681A228474E5E9DE CRC64;
                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-86034211; PubMed=3840489;
Sepito R.R., Lodish H.F.;
"Structure of the murine anion exchange protein.";
J. Cell. Biochem. 29:1-17(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 104; DB 1;
Pred. No. 4.4e-09;
splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                929 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                            POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                               POTENTIAL
  Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol. Chem. 262:8035-8040(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-85268011; Pubmed-2410791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 11-929 FROM N.A. MEDLINE-86274622; PubMed=3015590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                               103172 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 316:234-238(1985).
                                                                                                                                                                                                                                                                                                                        822
881
                                                                                                                                                                                                                                                                                                                                                                                                                                            927 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Palmi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                        641
677
715
779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLC4A1 OR AE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kopito R.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B3AT_MOUSE
```

4

```
B3AT_CHICK
    FFFFS
                                                                                                                                                                                                                                                                                                                                                                 A POPULAR TO THE POPU
                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                . 음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@iBb-sib.ch).
                                                                                                                                                                                                                                                                            ERYTHROCYTE MEMBRANE. BAND 3 HAS TWO FUNCTIONAL DOWAINS. ITS INTEGRAL DOMAIN MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS THE MEMBRANE, WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING STITES FOR CYTOSKELETAL PROTEINS, GLYCOLYTIC ENZYMES, AND HEMOGLOBIN.
                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY AND APPEARS TO BE TETRAMERIC. SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                   'Major proteolytic fragments of the murine band 3 protein as obtained
                                                                                                                    SEQUENCE OF 33-47; 360-375; 382-395 AND 578-590.
MEDLINE-89229233; PubMed-2713407;
Raida M., Wendel J., Kojro E., Fahrenholz F., Fasold H., Legrum B.,
Demuth D.R., Showe L.C., Ballantine M., Palumbo A., Fraser P.J., Cioe L., Rovera G., Curtis P.J.; "Cloning and structural characterization of a human non-erythroid
                                                                                                                                                                                                                    after in situ proteolysis.";
Biochim. Biophys. Acta 980:291-298(1989).
-1- FUNCTION: BAND 3 IS THE MAJOR INTEGRAL GLYCOPROTEIN OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. . .) (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Anion exchange; Erythrocyte; Lipoprotein; Palmitate; Alternative splicing.
DOMAIN 423 929 MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXOPLASMIC LOOP (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL. EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISOId-P04919-2; Sequence-VSP_000454;
TISSUE SPECIFIY: ERYTHROCYTE.
SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event-Alternative splicing; Named isoforms-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Erythrocyte;
IsoId=P04919-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:109399; Slc4al.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR001707; HCO3_cotranspt.
Pfan; PF00955; HCO3_cotranspt.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, X02677; CAA26506.1; -. EMBL, M29379; AAA37187.1; -. EMBL, J02756; AAA37278.1; -. EMBL, X03917; CAA27555.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "IGRFAMS; TIGR00834; ae; 1
                                                        band 3-like protein.";
EMBO J. 5:1205-1214(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                        ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44443
5529
5529
6621
6621
6642
737
737
737
737
737
737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A25314; A25314.
HSSP; P02730; 1BTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name-Kidney
                                                                                                                                                                                Passow H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY AND APPEARS TO BE TETRAMERIC.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: ENTYTROCYTE.
-!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACROSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Band 3 anion transport protein.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                     Gaps
                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 929;
                 Missing (in isoform Kidney).
/FTId=VSP_000454.
6 - S (IN REF. 5).
5 5C0E281C394FB614 CRC64;
                                                                                                                                     Indels
   PALMITATE (BY SIMILARITY)
                                                                                                   Score 104; DB 1;
Pred. No. 4.4e-09;
                                                                                                                                                                                                                                                                                                                    01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
                                                                                                                                     0; Mismatches
                                                                                                   100.0%; Score 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-89039870; PubMed=318555;
                                                                                                                                                                                      738 GMPWLSATTVRSVTHANALT 757
                                                                                                                                                                    1 GMPWLSATTVRSVTHANALT 20
                                                                                                                     100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M23404; AAA48753.1; -. HSSP; P02730; 1BTQ.
                                                                  103135
                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                        STANDARD;
861
79
                                                  467
                                                  467
929 AA;
                                                                                                                Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      417
450
473
504
536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEMOGLOBIN.
                                                                                                                                                                                                                                                                                      B3AT_CHICK
P15575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
TRANSMEM
TRANSMEM
               VARSPLIC
                                                                  SEQUENCE
                                                  CONFLICT
                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus
```

S

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics and the EMBL outstation—
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kudrycki K.E., Newman P.R., Shull G.E.;
"CDNA cloning and tissue distribution of mRNAs for two proteins that
are related to the band 3 Cl-/RCO3-exchanger.";
J Biol. Chem. 265:462-471(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
SLC4A2 OR AE2 OR B3RP2.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                          174 POTENTIAL.
152 PALMITAEL (BY SIMILARITY).
1546 N-LINKED (GLCNAC. .) (POTENTIAL).
1568 N-LINKED (GLCNAC. .) (POTENTIAL).
101893 MW; 37E163141FBDC16A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kopito R.R.; "Functional expression and subcellular localization of an anion exchanger cloned from choroid plexus."; Proc. Natl. Acad. Sci. U.S.A. 87:5278-5282(1990).
-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE DISTRIBUTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lindsey A.E., Schneider K., Simmons D.M., Baron R., Lee B.S.,
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
EXOPLASMIC LOOP (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 918;
                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXOPLASMIC LOOP (POTENTIAL).
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 95; LL ...
Pred. No. 1.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1234 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                         POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Stomach;
MEDLINE=90094439; PubMed=2294114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-90319095; PubMed-2371270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.3%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         918 AA;
```

```
159
                                                                                                   Name-C1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIPID
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RANSMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                  --
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         P13808; Q9ES09; Q9ES10; Q9ES11; Q9ES12; Q9ES13;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM A).
MEDILINE-99034212; PubMed=3182834;
Alper S.L., Kopito R.R., Libresco S.M., Lodish H.F.;
"Cloning and characterization of a murine band 3-related cDNA from kidney and from a lymphoid cell line.";
J. Biol. Chem. 263:17092-17099(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lecanda J., Urtasun R., Medina J.F.; ^*Molecular cloning and genomic organization of the mouse AE2 anion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
      HSSP; P02730; 1BTQ.
InterPro; IRR001717; Anion_exchange.
InterPro; IRR0013020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotranspt.
PRINTS; PR01231; HCO3TRNSPORT.
PRINTS; PR01231; HCO3TRNSPORT.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Transport; Antiport; Ion transport; Anion exchange; Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY MEDLINE-20462926; PubMed-11006093;
                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                          Score 93; DB 1; Length 1234;
                                                                                                                                              POTENTIAL. EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                         HIS-RICH.
N-LINKED (GLCNAC. . .) (POTE N-LINKED (GLCNAC. . . ) (POTE N-LINKED (GLCNAC. . . ) (POTE PALMITYEE (BY SIMILARITY).
G -> A (IN REF. 2)
                                                                                                                                                                                                                                                                                                              > I (IN REF. 2).
FAB4ED12BB916216 CRC64;
                                                                                                           MEMBRANE (ANION EXCHANGE)
                                                                                                                                                                          CYTOPLASMIC (POTENTIAL)
                                                                                                   CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem. Biophys. Res. Commun. 276:117-124(2000).
                                                                                                                                                                                                                                                                                                     -> I (IN REF. 2).
                                                                                                                                                                                                                                                                                            (IN REF.
                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                 POTENTIAL.
                                                                                                                      POTENTIAL.
                                                                                                                             POTENTIAL.
                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                              o PG
                                                                                                                                                                                                                                                                                                                                                                                        ŗ
                                                                                                                                                                                                                                                                                                                                                                             1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                         89.4%;
85.0%;
                                                                                                                                                                                                                                                                                                                        136635
                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLC4A2 OR AE2.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                              1156 11:
1234 AA;
PIR; A34911; A34911
                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exchanger gene.
                                                                                                                                                                                                                                         DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                           DOMAIN
TRANSMEM
                                                                                                                                                                                                              TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                  FRANSMEM
                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                              TRANSMEM
                                                                                                                                                                                    PRANSMEM
                                                                                                                                                                                             FRANSMEM
                                                                                                                             FRANSMEM
                                                                                                                                        TRANSMEN
                                                                                                                                                                                                      PRANSMEN
                                                                                                   DOMAIN
                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                            LIPID
                                                                                                                                                                                                                                                                                                                                                           Matches
ò
                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: isoform a is widely expressed at similar levels in all tissues examined. Isoforms bl and b2 are predominantly expressed in stommach although they are also detected at lower levels in other tissues. Isoform c1 is stommach-specific. Isoform c2 is expressed at slightly higher levels in lung and stommach than in other tissues. SIGNIANTY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PALMITATE (BY SIMILARÍTY).
MSSAPRRPASGADSLHT -> MDFLLRPQ (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane; Glycoprotein; Transport; Antiport; Ion transport; Andion exchange; Lipoprotein; Palmitate; Alternative splicing. DOMAIN 1 CYTOPLASMIC (POTENTIAL).

MEMBRAIN 704 . 1237 MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL. EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P13808-5; Sequence=VSP_000459, VSP_000461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                       SUBCELLULAR LOCATION: Integral membrane protein. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GLCNAC. . .)
                                                                                                                                    Event=Alternative splicing; Named isoforms=5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GLCNAC.
                                                                                                                                                                                                                                                                                                                                     IsoId=P13808-3; Sequence=VSP_000457;
                                                                                                                                                                                                                                                                      IsoId=P13808-2; Sequence=VSP_000458;
                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=P13808-4; Sequence-VSP_000460;
                                                                                                                                                                                                   IsoId=P13808-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IIGRFAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIS-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:109351; S1c4a2.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfan; PF00955; HCO3_cotranspt.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AF255774; AAG23154.1; -.
EMBL, AF255774; AAG23155.1; -.
EMBL, AF255774; AAG23156.1; -.
EMBL, AF255774; AAG23158.1; -.
EMBL, AF255774; AAG23157.1; -.
PIR; A31789; A31789.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J04036; AAA65505.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P02730; 1BTQ.
```

B2). /FTId-VSP_000457

```
DOMAIN
                                                                                                                                                                                                                                                                                RESULT 9
                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                        ö
                                                  /FTIG-VSP_000466.
ERTSPSPPTQTPHQEAAPRASKGAQTG -> MPAFQEWKSG
GLREEAVFGAHGCSVCR (in isoform C2).
 MSSAPRRPASGADSLHT -> MTQ (in isoform B1).
                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                             01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
                                                                                                                                                                                                                                                                                                                                   Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane: Glycorotein; Transport; Antiport; Ion transport; Anion exchange; Lipoprotein; Palmitate.
DOMAIN 104 127 CYTOPLASMIC (POTENTIAL).
DOMAIN 704 127 POTENTIAL.
TRANSMEM 733 770 POTENTIAL.
TRANSMEM 733 770 POTENTIAL.
TRANSMEM 730 812 POTENTIAL.
TRANSMEM 822 843 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                   DECENTAIN—New Zealand white;
MEDLINE-93035730; PubMed-1415547;
Chow A., Dobbins J.W., Aronson P.S., Igarashi P.;
"CDNA cloning and localization of a band 3-related protein from
                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Am. J. Physiol. 263:G345-G352(1992).
-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
DISTRIBUTION.
                                                                                                                                  Length 1237;
                                                                                                                                                        1; Indels
                                                                                  /FTIG=VSP_000461.
A -> G (IN REF. 2).
W; 1A0782C0071782EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
           /FTId=VSP_000458.
Missing (in isoform C2).
                              /FTId=VSP_000459.
Missing (in isoform C1).
                                                                                                                                 DB 1; L
3.7e-07;
                                                                                                                                                                                                                                                         PRT; 1237 AA.
                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGREAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                  Score 93;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P02730; 1BTQ.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR00300; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotranspt.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                         1046 GLPWLAAATVRSVTHANALT 1065
                                                                                                                                                                            1 GMPWLSATTVRSVTHANALT 20
                                                                                                            136813 MW;
                                                                                                                                 89.4%;
85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; S45791; AAB23488.1; -. PIR; A56764; A56764.
                                                                                                                         Ouery Match
Best Local Similarity 85.09
                                                                                                                                                                                                                                                         STANDARD;
                      166
                                           198
                                                                                                205
17
                                                                 193
                                                                                                205 20
1237 AA;
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9986;
                                                                167
                                                                                                                                                                                                                                                                                                                           SLC4A2 OR AE2
                                                                                                                                                                                                                                                         B3A2_RABIT
                                                                                                CONFLICT
 VARSPLIC
                      VARSPLIC
                                           VARSPLIC
                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1leum."
                                                                                                                                                                                                                                               B3A2_RABIT
                                                                                                                                                                                                                                    RESULT 8
                                                                                                                                                                                                                                                                   g
 89
                                                                                                                                                                              ď
```

```
A REDINE-22388257; PubMed-12477932;

A Strausberg R.L. Feingold E.A. Grouse L.H., Derge J.G.,

A Itausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Robards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Scheni J.E., Jones S.J.M., Mara M.A.;

Reneration and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B3A2_HUMAN STANDARD; PRT; 1241 AA.
P04920; Q59613;
13-AUG-1987 (Rel. 05, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (BND3L).
SLC4A2 OR AE2 OR EPB3L1 OR HKB3 OR MPB3L.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 375-1241 FROM N.A.
MEDLINE-86274622; PubMed-3015590;
Demuth D.R., Showe L.C., Ballantine M., Palumbo A., Fraser P.J.,
                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
PALMITAE (BY SIMILARITY).
W; 2811D11051552B82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM A).
MEDLINE-92223115; PubMed-1562608;
Gehrig H., Mueller W., Appelhans H.;
"Complete nuclectide sequence of band 3 related anion transport protein AE2 from human kidney.";
                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                    Score 93; DB 1; Length 1237;
Pred. No. 3.7e-07;
2; Mismatches 1; Indels
EXOPLASMIC LOOP (POTENTIAL)
                                             CYTOPLASMIC (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochim. Biophys. Acta 1130:326-328(1992)
                                                                                                                  POTENTIAL. POTENTIAL.
                                                                                                                                                                   POTENTIAL.
PRO-RICH.
                                                                                              POTENTIAL
                                                                                                                                                                                                                   HIS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1046 GLPWLAAATVRSVTHANALT 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM B1).
                                                                                                                                                                                                                                                                                                                                         136535 MW;
                                                                                                                                                                                                                                                                                                                                                                                         89.4%;
85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
896
914
929
929
11006
1132
11132
11195
88
88
855
864
878
878
                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                    864
878
1169
                                                                                                                  1032
1087
1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Brain;
                                                                                                                                                                                                                                                                    CARBOHYD
CARBOHYD
                      TRANSMEM
DOMAIN
                                                                                           TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                  TRANSMEM
                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B3A2_HUMAN
                                                                                                                                                                                                                                                                                                                       LIPID
```

œ

```
450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLC4A3 OR AE3.
                                                                                                                                                                                                                                                                                                                                                                     B3A3_MOUSE
P16283;
                CONFLICT
                                                 CONFLICT
                                                                   CONFLICT
                                                                                                      CONFLICT
                                                                                                                                     SEQUENCE
                                                                                                                                                                            Query Match
                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                      B3A3_MOUSE
                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                      RESULT 10
                                                                                                                                                                                                                                                                                                                                                                         HID DRAW RECORDED TO THE PROPERTY OF THE PROPE
                  SELEFFF
                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PALMITATE (BY SIMILARITY).
MSSAPRLPAKGADSFCT -> MTQ (in isoform B1).
                                                                                                                                                                                                                                                                                                                                                                                                                                REMEL; X62137; CA444067.1; -
REMEL; BC009386; AAH09386.1; -
REMEL; BC009344; AAH09386.1; -
REMEL; BC009344; AAH09386.1; -
REMEL; X03918; CAA27556.1; -
REMEL; X03918; CAA27556.1; -
REMEL; X03918; CAA27556.1; -
REMEL; X03918; CA427556.1; -
REMEL; X03918; CA427556.1; -
REMEL; X03918; CA427556.1; -
REMEL; X030186; S21086.
REMEL; X03008509; F: anion transporter activity; TAS.
REMEC; GO:0006820; F: anion transport; TAS.
REMEC; GO:0006820; F: anion transport; TAS.
REMEC; GO:0006820; P: anion transport; TAS.
REMEC; REMO32017; Anion_exchange.
REMEC; REMO32019; ANION_EXCHANGER.1; 1.
REMEC; REMO32019; ANION_EXCHANGER.2; 1.
REMEC; REMO32019; ANION_EXCHANGER.2; 1.
REMEC; REMEC; REMO32019; ANION_EXCHANGER.2; 1.
REMEMEL; REMEMEC; REMEMER, SALICETNATIVE SPLICING.
TOWAIN TO DOMAIN TO REMEMBRANE (ANION EXCHANGE).
THE MANNAY TO SALIAME TO SALIAME (ANION EXCHANGE).
Cioe L., Rovera G., Curtis P.J.;
"Cloning and structural characterization of a human non-erythroid band 3-like protein.";
EMBO J. 511205-1214(1986).
-:- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE DISTRIBUTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL). (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                                                                                                                                              ISOId=P04920-2; Sequence=VSP_000456; SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
                                                                                                                   SUBCELLULAR LOCATION: Integral membrane protein. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLCNAC. . .)
                                                                                                                                                         Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -> M (IN REF. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GIN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /FTId=VSP_000456
                                                                                                                                                                                                             IsoId=P04920-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
POTENTIAL.
POTENTIAL.
PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lipoprotein; F
707
1241 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1010
1059
1136
11199
320
859
868
868
882
11173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68
74
92
1122
1157
248
399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1091
1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           859
868
882
                                                                                                                                                                                                                               Name-B1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                       ö
LLGHHHGQGAESDPHVTEPLMGGVPE -> CWGITMVRGLR
                     VTPTSPSLSWEVFLR (IN REF. 3).
EL -> DV (IN REF. 1 AND 3).
AAGAAEDDPLRRTGRP -> RGGQLKMIPSADGAA (IN REF. 1 AND 3).
Q -> R (IN REF. 1 AND 3).
L -> P (IN REF. 1 AND 3).
Mw; B116908C5A71DB77 CRC64;
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-90075236; Pubmed-2686841;
Kopito R.R., Lee B.S., Simmons D.M., Lindsey A.E., Morgans C.W.
                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Morgans C.W., Kopito R.R.; "Generation of truncated brain AE3 isoforms by alternate mRNA processing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schneider K.;
"Regulation of intracellular pH by a neuronal homolog of the erythrocyte anion exchanger.";
cell 59:927-937(1989).
                                                                                                                                                                                                                                 Score 93; DB 1; Length 1241; Pred. No. 3.7e-07;
                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 3 (Neuronal band 3-like protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=P16283-3; Sequence=VSP_000466, VSP_000467; -:- TISSUE SPECIFICITY: NEURONAL. -:- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=P16283-2; Sequence=VSP_000464, VSP_000465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING MEDLINE=94171936; Pubmed=8126106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1227 AA
                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=P16283-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P02730; IBTQ.
MGD; MGI:109350; Slc4a3.
InterPro; IPR001717; Anion_exchange.
                                                                                                                                                                                                                                                                                                                                                                  1050 GLPWLAAATVRSVTHANALT 1069
                                                                                                                                                                                                                                                                                                                                          1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M28383; AAA37184.1; -. EMBL; S69314; AAB30140.1; -.
                                                                                                                                                                                 136966
                                                                                                                                                                                                                                    89.4%;
                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                   486
                                                                                                                           824
902
                                                                                                                           824 82
902 90
1241 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A33638; A33638.
                                                                                                                                                                                                                                                       Local Similarity
es 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=311-AE3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=FL-AE3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=14-AE3;
```

```
CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                             POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-PRO.
POLY-LYS.
                                                                                                                   hastronia proposition in the proposition of the pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |:|||:| ||||||| |||||
1037 GLPWLTAATVRSVTHVNALT 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM BAE3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GMPWLSATTVRSVTHANALT
                                                                            EMBL; J05167; AAA40798.1; -. PIR; B34911; B34911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.6%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                      1123
1186
868
1160
                                                                                                                                                                                                                                                                                                                                                                                                        997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                            HSSP; P02730; 1BTQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B3A3_HUMAN
P48751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                             PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                              RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                        RANSMEN
                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B3A3_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2
   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                   Missing (in isoform 311-AE3).
/FIId-VSP_000465.
KPLHMPGGDGHRGKSLK -> FCVLRSPSPCLGETVTEGKA (in isoform 14 AE3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AALLDLEOTTL -> RAFWAGNESLL (in isoform
                                                                                         Transmembrane; Glycoprotein; Transport; Antiport; Ion transport; Anion exchange; Lipoprotein; Palmitate; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 89; DB 1; Length 122
Pred. No. 1.66-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Missing (in isoform 14-AE3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
28-FCB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 3 (Neuronal band 3-like protein).
SLC4A3 OR AB3 OR B3RP3.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'FTId=VSP_000467.
                                                                                                                                        MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- TISSUE SPECIFICITY: NEURONAL.
-i- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (F
PALMITATE (BY SIMILARITY)
                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                      FTIG=VSP_000464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'FTId=VSP_000466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1227 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                           CYTOPLASMIC
                                                                                                                                                                                                                                                                                                           POTENTIAL. POLY-GLU.
                                         TICRFAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                           311-AE3
IPR003020; HCO3_cotranspt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1227 AA; 135164 MW;
                            PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.6%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                      1227
                                                                                                                                                                                                                                                                                           1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                   503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
es 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                      392
                                                                                                                                                                                                                                                                                                                                                                                                                                                   487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  504
                                                                                                                                      DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B3A3_RAT
                                                                                                                                                                                                                 PRANSMEM
                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                      VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                      FRANSMEM
                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                         VARSPLIC
                                                                                                                                                                                    PRANSMEM
                                                                                                                                                                                                     FRANSMEM
                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                        DOMAIN
                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               å
```

```
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 3 (Neuronal band 3-like protein) (Cardiac/brain band 3-like protein) (CAE3/BAE3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                TIGRFAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
Anion exchange, Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Heart;
MEDLINE-55008042; PubMed-7923606;
Yannoukakos D., Stuart-Tilley A., Fernandez H., Fey P., Duyk G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . LALMITATE (BY SIMILARITY).
HIS-PACH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular cloning, expression, and chromosomal localization of isoforms of the AE3 anion exchanger from human heart."; Circ. Res. 75:603-614(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 89; DB 1; Length 1227;
Pred. No. 1.6e-06;
Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-LEU.
W; 3EB1620EE011730E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1232 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
```

```
PRANSMEM
                                                                                                                                                                                                                                                               B3A3_RABIT
                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                   RESULT 13
  셤
                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                         R MIM; 106195; -.

R GO: 6001608887; C: integral to plasma membrane; TAS.

R GO: 600160524; C:membrane fraction; TAS.

R GO: 600160524; C:membrane fraction; TAS.

R GO: 600160522; F:inorganic anion exchanger activity; TAS.

R InterPro: IPR00177; Anion_exchange.

R InterPro: IPR00171; Anion_exchange.

R InterPro: IPR001320; HCO3_cotranspt.

R InterPro: IPR00320; HCO3_cotranspt.

R Ffam; PF00955; HCO3_cotranspt.

R Ffam; PF00955; HCO3_cotranspt.

R Ffam; PR00121; HCO3TRNSPORT.

R TIGREAMS; TIGR00834; ae; 1.

DR ROSITE; PS00220; ANION_EXCHANGER_1; 1.

DR ROSITE; PS00220; ANION_EXCHANGER_2; 1.

KW Transmembrane; Glycoprotein; Transport; Anion exchange; Lipoprotein; Palmitate; Alternative splicing.
                  Kudo S., Mattel M.-G., Bloor C.M., Fukuda M., Ranney H.M., Xu A.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
DISTRIBUTION. MEDIATES AT LEAST A PART OF THE CL(-)/HCO3(-)
EXCHANGE IN CARDIAC MYOCYTES. BOTH BAE3 AND CAE3 FORMS TRANSPORT
                                                                                                                                                           ISOId=P48751-2; Sequence=VSP_000462, VSP_000463;
TISSUE SPECIFICITY: BOTH BAE3 AND CAE3 ARE EXPRESSED IN FAILING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -> MPA (in isoform CAE3).
Id=VSP_000463.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Missing (in isoform CAE3)./FTId=VSP_000462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEMBRANE (ANION EXCHANGE)
                                                                                                                                                                                  VENTRICLE. SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL)
                                                                                   SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                             ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms-2;
Comment-Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -> V (IN REF. 2).
                                                                                                                                       IsoId=P48751-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
POTENTIAL.
POLY-GLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PALMITATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /FTIG=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRO-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-LYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY - LEU
SEQUENCE FROM N.A. (ISOFORM CAE3).
                                                                                                                                                                                                                                                                                                   EMBL; U05596; AAA50748.1; -. EMBL; L27213; AAB05850.1; -. PIN; 138496; 138496. Genew; HGSP; 11029; SLC4A3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1002
1049
1128
1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304
343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .083
155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297
                                                                                                                              Name=BAE3;
                                                                                                                                                   Name=CAE3
          rissue=Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /ARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                   This
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00219; ANION, EXCHANGER 1; 1.
PROSITE; PS00220; ANION_EXCHANGER 2; 1.
Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
Anion exchange; Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 3 (Neuronal band 3-like protein) (Anion exchanger 3 brain isoform).
                                                                                                                                                                                                                                                                                   Length 1232;
                                                                                                                                                           -> G (IN REF. 2).
-> E (IN REF. 2).
-> E (IN REF. 2).
-> P (IN REF. 2).
-> M (IN REF. 2).
1825BE15977C3821 CRC64;
                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Abuladze N., Pushkin A., Kurtz I.; Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: NEDRONAL.
-!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEMBRANE (ANION EXCHANGE)
    REF. 2).
REF. 2).
REF. 2).
IN REF. 2).
REF. 2).
                                                                                                                                                                                                                                                   Score 89; DB 1; Leng.
                                                                                                           KEF. 2).
(IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1233 AA.
P -> S (IN REF
D -> G (IN REF
D -> G (IN REF
GS -> F (IN REF
F -> L (IN REF
EGSLA -> D (IN REF
S -> C (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HC03_cotranspt.
                                                                                                                                                               ^ ^ ^
                                                                                                                                                                                                                                                                                                                                                                                        |:|||:| ||||||| |||||
1042 GLPWLTAATVRSVTHVNALT 1061
                                                                                                                                                                                                                          ^
                                                                                                                                                                                                                                             MM;
                                                                                                                                                                                                                                                                                                                                                                     1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00955; HC03_cotransp; 1.
PRINTS; PR01231; HC03TRNSPORT.
                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF031650; AAB86859.1; -
                                                                                                                                                                                                                                                                                   85.6%;
80.0%;
                                                                                                                                                                                                                                             1232 AA; 135706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR01231; HCO3TRNSF
TIGREAMS; TIGR00834; ae; 1
                                                                                                                                                                                                                                                                                                    Local Similarity 80.0 nes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P02730; 1BTQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      710
738
795
827
894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLC4A3 OR AE3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B3A3_RABIT
018917;
                                                                                                                                                                                                                        CONFLICT
                                                            CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
TRANSMEM
                                          CONFLICT
                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRANSMEM
```

```
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
RALINKED (BY SIMILARIY).
WW. FA1739862ED5ADBF CRC64;
                                                                                                                                   N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                              Score 83; DB 1; Length 1238;
Pred. No. 1.6e-05;
2; Mismatches 2; Indels
                                     EXOPLASMIC LOOP (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
         POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                            POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
PRO-RICH.
                                                                 POTENTIAL
                                                                                                                             HIS-RICH.
                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                1047 GLLWLAAATVRSVTHANALT 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21269379; PubMed=11102437;
                                                                                                                                                                                                                                      1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                      B3A4_RABIT STANDARD; E Q9GKY1; Q9GKY2; 15-SEP-2003 (Rel. 42, Last seq. 15-SEP-2003 (Rel. 42, Last seq. 15-SEP-2003 (Rel. 42, Last annotation)
                                                                                                                                                                                                79.8%;
80.0%;
                                                                                                                                                                            137358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=2; Synonyms=AE4b;
                                                                                                                                                                                                Query Match 79.8
Best Local Similarity 80.0
Matches 16; Conservative
728
771
813
844
897
915
930
951
1007
11133
11196
                                                                                                                            88
856
865
879
                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9986;
                                                                                     1033
1088
1160
                                                                                                                                                                   1170
1238
                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Kidney
                                                                                                                                                                            SEQUENCE
                                                                                                                                       CARBOHYD
                                                                                                                                                           CARBOHYD
                                                TRANSMEM
                                                                   TRANSMEM
                                                                                                         TRANSMEM
                                                                                                                                                CARBOHYD
                             TRANSMEM
                                                                             TRANSMEM
                                                                                      TRANSMEM
                                                                                                TRANSMEM
           TRANSMEN
                  TRANSMEM
                                       DOMAIN
                                                                                                                    DOMAIN
                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                B3A4_RABIT
                                                                                                                                                                                                                                                                                       RESULT 15
                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@libersib.ch).
                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                    % CCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
18-PEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (AE2 anion exchanger).
                                                                                                                                                                                                                                                                                                                                              Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00955; HCO3_cotranspt.
PRINTS; PR01231; HCO3_ratransp; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00219; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Transport; Antion exchange; Lipoprotein; Transport; Anion exchange; Lipoprotein; Palmitate.
DOMAIN 1 704 CYTOPIASMIT COMPUTATION
                                                         N-LINKED (GLCNAC. . .) (POTENTIAL).
PALMITATE (BY SIMILARITY).
                                                                                                                                                                             ;
0
                                                                                                                                                         Length 1233;
                                                                                                                                                Score 89; DB 1; Length 123.
Pred. No. 1.6e-06;
                                                                                                                                     AE486423E9818583 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL). MEMBRANE (ANION EXCHANGE)
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                     PRT; 1238 AA.
                                      POTENTIAL
                                                POTENTIAL
                                                                             HIS-RICH.
POLY-GLU.
                                                                                                         POLY-LYS.
                                                                                                                    POLY-SER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HC03_cotranspt.
                                                                                                                                                                                                           1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF121253; AAD19700.1; -.
                                                                                                                                                          85.6%;
                                                                                                                                      AA; 135759
                                                                                                                                                                   80.08;
                                                                                                                                                                    Local Similarity 80.0 tes 16; Conservative
                                                                                                                                                                                                                                                                    STANDARD;
                    1003
1050
1129
1192
874
874
1166
83
                                                                                                         312
446
1188
                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10141;
                                                                                                                   443
1185
1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P02730;
                                                                                                                                                                                                                                                                                                                                     SLC4A2 OR AE
                                                                                                                                                                                                                                                                 B3A2_CAVPO
Q9Z0S8;
                                               TRANSMEM
CARBOHYD
LIPID
                  TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                            Query Match
                                                                                                                                       SEQUENCE
           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                             DOMAIN
                                                                                        DOMAIN
                                                                                                DOMAIN
                                                                                                         DOMAIN
                                                                                                                    DOMAIN
                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                           B3A2_CAVPO
                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                RESULT 14
                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                   셤
```

ö

Gaps

.; 0

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISOId-03GKYI-2; Sequence-VSP_007088;
--- TISSIE SPECIFICITY: Highly expressed in kidney. Expressed in certain types of cells in the kidney cortex.
--- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eut
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       kidney cells.
-!- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
Name=1; Synonyms=AE4a;
IsoId=Q9GKYI-1; Sequence=Displayed;
                                                                                      15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Anion exchange protein 4 (Anion exchanger 4).
CLGA9 OR AE4.
Oryctolagus cuniculus (Rabbit).
955 AA.
```

```
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                     HSSP; P02730; 1BNX.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR0031717; Anion_exchange.
InterPro; IPR00320; HCO3_cotransp.
Pfan; PF00955; HCO3_cotransp; 1.
PRINTS; PR01231; HCO3TRNSPORT.
TRIRRAMS; TGR00834; ac; 1.
Transmembrane; Glycoprotein; Transport; Antiport; Ion transport; Anion exchange; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          871 891 POTENTIAL.
548 548 N-LINED (GLCNAC. . ) (POTENTIAL).
572 572 N-LINED (GLCNAC. . .) (POTENTIAL).
317 332 Missing (in isoform 2).
/FTIGH-VSP_007088.
955 AA; 105032 MW; 04E595A2BFC415B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.1%; Score 49; DB 1; Length 955; ilarity 42.1%; Pred. No. 4.2; Conservative 5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                                                                                                                         CYTOPLÁSMIC (POTENTIAL).
MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL). POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GMPWLSATTVRSVTHANAL 19
                                           EMBL; AB038263; BAB18935.1; -. EMBL; AB038264; BAB18936.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
TRANSMEM
TRANSMEM
TRANSMEM
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                   PRANSMEM PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
IRANSMEM
IRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                          RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
```

Search completed: September 3, 2003, 11:46:55 Job time: 10.25 secs

744 GLPWYVSATVLSLAHMDSL 762

us-10-087-464-2.rsp

Page 1

```
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

September 3, 2003, 11:25:42; Search time 9.25 Seconds
(without alignments)
101.679 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-087-464-2 98 1 SVTHANALTVMGKASTPGAA 20

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	homod	rattu	PO4919 mus musculu	P23347 rattus norv	æ	P48746 oryctolagus		0 homo sa	'n	-	P16283 mus musculu	P23348 rattus norv	_	_	P4447 haemophilus		P14914 rickettsia	Q53047 r outer mem			Q8wv16 homo sapien		Q8uey3 agrobacteri	-	P33025 escherichia	Q92210 candida alb	Q10821 mycobacteri	Q61140 mus musculu		P54189 plasmodium	œ	9118 cephalos	P46596 candida alb
SUMMARIES	ID	B3AT_HUMAN	B3AT_RAT	B3AT_MOUSE	B3A2_RAT	B3A2_MOUSE	B3A2_RABIT	B3A2_CAVPO	B3A2_HUMAN	B3AT_CHICK	B3AT_ONCMY	B3A3_MOUSE	B3A3_RAT	B3A3_HUMAN	B3A3_RABIT	Y003_HAEIN	OMPB_RICCN	120K_RICRI	OMPB_RICRI	NUCL_HUMAN	FTSY_RICPR	WD21_HUMAN	YFC5_SHEFR	TPIS_AGRT5	PANB_OCEIH	YEIN_ECOLI	PUR6_CANAL	YT00_MYCTU	BCA1_MOUSE	BCA1_RAT	PBP_PLAFA	BRS3_MOUSE	o	OPS4_CANAL
	Length DB	911 1			1234 1									1232 1						706 1				256 1			568 1					66	C)	0
ď	Query Match	100.0	92.9	95.9	74.5	74.5	74.5	74.5	74.5	72.4	64.3	62.2	62.2	62.2	62.2	20.0	49.0	48.0	48.0	43.4				41.8	40.8	。	ö	ö		ö	ó	39.8	σ.	σ.
	Score	86	91	91	. 73	73	73	73	73	. 71	63	61	61	61	61	49	48	47		42.5	42	41.5	41	41	40	40	40	40	40	40	39	33	39	39
	Result No.	1	7	m	4	'n	9	7	ω .	on (10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	78	29	30	31	32	33

bacillus su	P94368	YXKO_BACSU	7	276	∞.	38	38	45
rickettsia	Q9zcs7	RS13_RICPR	Н	125	ω.	38	38	44
rickettsia	Q929y8	RS13_RICCN	7	125	ω,	38	38	43
brachydanio	004475	B2MG_BRARE	Н	116	8	38	38	42
human herpe	P52441	UL49_HSV6U	~	470	m.	33	38.5	41
homo sapien	015782	·C3L2_HUMAN	Н	390	٣.	39	38.5	40
methanosarc	. Q8tjul	EGSA_METAC	Н	356	39.3	39	38.5	39
homo sapien	016799	RTN1_HUMAN	Н	176	ω.	39	39	38
homo sapien	. 016650	TBR1_HUMAN	7	682	ω.	39	39	37
mus musculu	064336	TBR1_MOUSE	Н	. 681	ω.	39	36	36
xenopus lae	005049	MUC1_XENLA	Н	662	ω.	39	39	35
caenorhabdi	011178	YPC1_CAEEL	Т	529	ω.	39	39	34
		•						

ALIGNMENTS

~

```
Brunati A.M., Bordin L., Clari G., James P., Quadroni M., Baritono E.,
Pinna L.A., Donella-Deana A.;
                                                                                                                                                                                                                                                                                                                                                                                              "Sequential phosphorylation of protein band 3 by Syk and Lyn tyrosine kinases in intact human erythrocytes: identification of primary and
                                                                            ï.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ٦,
conformation and a possible molecular mechanism for anion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT HE 400-ALA--ALA-408 DEL, AND VARIANT MEMPHIS GLU-56.
MEDLINE-92107882; PubMed=1722314;
Jarolin P., Palek J., Amato D., Hassan K., Sapak P., Nurse G.T.,
Rubin H.L., Zhai S., Sahr K.E., Liu S.-C.;
"Deletion in erythrocyte band 3 gene in malaria-resistant Southeast
Asian ovalocytosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92167271; PubMed=1538405;
Schoffield A.E., Tanner M.J.A., Pinder J.C., Clough B., Bayley P.M.,
Nash G.B., Dluzewski A.R., Reardon D.M., Cox T.M., Wilson R.J.M.,
Gratzer W.B.;
"Basis of unique red cell membrane properties in hereditary
                                                                                                                                                                                                                                                    Okubo K., Hamasaki N., Hara K., Kageura M.;
"Palmitoylation of cysteine 69 from the COOH-terminal of band 3
protein in the human erythrocyte membrane. Acylation occurs in the
middle of the consensus sequence of F-I-IICLAVL found in band 3
protein and G2 protein of Rift Valley fever virus.";
J. Biol. Chem. 266:16420-16424(1991).
                                                          MEDLINE-88228050; PubMed-3372523;
Kawano Y., Okubo K., Tokunaga F., Miyata T., Iwanaga S., Hamasaki
"Localization of the pyridoxal phosphate binding site at the COOH-
terminal region of erythrocyte band 3 protein.";
J. Biol. Chem. 263:8232-8238(1988).
                                                                                                                                     ROLE OF GLU-681, AND SEQUENCE.OF 665-688.
MEDLINE=92332495; PubMed=1352774;
Jennings M.L., Smith J.S.;
Jennings M.L., Smith J.S.;
Parlion-proton cotransport through the human red blood cell band 3 protein. Role of glutamate 681.";
J. Biol. Chem. 267:13964-13971(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Band 3 Tuscaloosa: Pro-327-->Arg substitution in the cytoplasmic domain of exythrocyte band 3 protein associated with spherocytic hemolytic anemia and partial deficiency of protein 4.2."; Blood 80:523-529(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT MEMPHIS GLU-56.

MEDLINE-91329825; PubMed-1678289;
MEDLINE-91329825; PubMed-1678289;
Yannoukakos D., Vassaur C., Driancourt C., Blouquit Y., Delauney Wajcman H., Bursaux E.;
"Human erythrocyte band 3 polymorphism (band 3 Memphis):
protein chemistry methods.";
Plood 78:1117-1120(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-92329950; PubMed-1378323;
Jarolim P., Palek J., Rubin H.L., Prchal J.T., Korsgren C.,
                                                                                                                                                                                                                                                                                                                                             PHOSPHORILATION OF TYR-8; TYR-21; TYR-359 AND TYR-904 MEDLINE=20400020; PubMed-10942405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Natl. Acad. Sci. U.S.A. 88:11022-11026(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                         secondary phosphorylation sites.";
Blood 96:1550-1557(2000).
                                                                                                                                                                                                                             PALMITOYLATION OF CYS-843.
MEDLINE=91358422; Pubmed=1885574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARÍANT HS LEU-868.
MEDLIŅE-93343855; PubMed-8343110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ovalocytosis.";
J. Mol. Biol. 223:949-958(1992).
[15]
                      Biochem. J. 213:577-586(1983)
                                                  OF 834-911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT HS ARG-327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cohen C.M.;
 sedneuce,
              exchange
                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                  101
```

```
VARIANTS HS GLN-760; TRP-760; CYS-808 AND TRP-870.
MEDLINE=95134893; PubMed=7530501;
Jarolinm P., Rubin H.L., Brabec V., Chrobak L., Zolotarev A.S.,
Alper S.L., Brugnara C., Wichterle H., Palek J.;
"Mutations of conserved arginines in the membrane domain of erythroid band 3 lead to a decrease in membrane-associated band 3 and to the phenotype of hereditary spherocytosis.";
Blood 85:634-640(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                 "Human erythrocyte protein 4.2 deficiency associated with hemolytic anemia and a homozygous 40 glutamic acid-->lysine substitution in the cytoplasmic domain of band 3 (band 3Montefiore)."; Blood 81:2155-2165(1993).
Bruce L.J., Kay M.M., Lawrence C., Tanner M.J.; "Band 3 HT, a human red-cell variant associated with acanthocytosis and increased anion transport, carries the mutation Pro-868-->Leu in the membrane domain of band 3."; Biochem. J. 293:317-320(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bozon M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT HS ASP-771.
MEDLINE=96136073; PubMed=8547122;
Maillet P., Vallier A., Reinhart W.H., Wyss E.J., Ott P., Texier P.,
Baklouti F., Tanner M.J., Delaunay J., Alloisio N.;
"Band 3 Chur: a variant associated with band 3-deficient hereditary
spherocytosis and substitution in a highly conserved position of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT BLOOD GROUP DI(A)/MEMPHIS-II.

WEDLINE-94266802. PubMed-8206915.

Bruce L.J., Anstee D.J., Spring F.A., Tanner M.J.;

Band 3 Memphis variant II. Altered stilbene disulfonate binding a the Diego (Dia) blood group antigen are associated with the human erythrocyte band 3 mutation pro-854-->Leu.";

J. Biol. Chem. 269:16155-16158(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T., Dornwell M., Herbers J., Kugler W., Oezcan R., Pekrun A., Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.; "Ankyrin-1 mutations are a major cause of dominant and recessive hereditary spherocytosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-97351102; PubMed-9207478;
Alloisio N., Texier P., Vallier A., Ribeiro M.L., Morle L., Bozon
Bursaux E., Maillet P., Goncalves P., Tanner M.J., Tamagnini G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Changes in the blood group Wright antigens are associated with mutation at amino acid 658 in human erythrocyte band 3: a site cinteraction between band 3 and glycophorin A under certain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Characterization of 13 novel band 3 gene defects in hereditary spherocytosis with band 3 deficiency."; Blood 88:4366-4374(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jarolim P., Murray J.L., Rubin H.L., Taylor W.M., Prchal J.T., Ballas S.K., Snyder L.M., Chrobak L., Melrose W.D., Brabec V.,
                                                                                                                                                                                                                                                                           MEDLINE-93229758; PubMed-8471774;
Rybicki A.C., Qiu J.J.H., Musto S., Rosen N.L., Nagel R.L.,
Schwartz R.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bruce L.J., Ring S.M., Anstee D.J., Reid M.E., Wilkinson S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANTS HS ASP-285; GLU-455; PRO-707; PRO-834 AND MET-837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANTS HS LYS-'40; CYS-518 AND MET-663 DEL.
MEDLINE-96225450; PubMed-8640229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Br. J. Haematol. 91:804-810(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT BLOOD GROUP WR(A).
MEDLINE=95111140; PubMed=7812009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97099297; PubMed=8943874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANTS HS SER-147 AND MET-488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genet. 13:214-218(1996).
                                                                                                                                                                                                                                                      VARIANT MONTEFIORE LYS-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transmembrane segment 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conditions.";
Blood 85:541-547(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fanner M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Palek J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
```

 $\boldsymbol{\alpha}$

```
Alternative splicing
                                                                                                                                                                                                                                                                                                    Best_Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 316:234-238(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
 Palmitate:
               420
927
441
441
527
528
558
604
619
                                                                                                                                                                   735
796
822
881
658
859
79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
                                                                                                                                                                                                                                                                 927 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLC4A1 OR AE1
 Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kopito R.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                          B3AT_MOUSE
P04919;
                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                          TRANSMEM
                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                         VARSPLIC
                                                                                                                                                                                                                                                                                         Query Match
                                                                                  TRANSMEM
                                                                                                                                                          TRANSMEM
                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                       TRANSMEM
                                    FRANSMEM
                                               TRANSMEM
                                                            TRANSMEM
                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                  TRANSMEM
                                                                       TRANSMEM
                                                                                                                       DOMAIN
                         DOMAIN
                                                                                               DOMAIN
                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                             B3AT_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MEB3)
                                                                                                                                                                                                                               LIPID
 ð
                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                   ö
                                                                                                                                                                                                                                                                                                                                                                                              KUDTYCKI K.E., Shull G.E., Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.

-!-FUNCTION: BAND 3 HAS TWO FUNCTIONAL DOMAINS: ITS INTEGRAL DOMAIN MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS THE MEMBRANE, WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING SITES FOR CYTOSKELETAL AND OTHER PROTEINS (BY SIMILARITY).

-!- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY
                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND APPEARS TO BE TETRAMERIC.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. IN THE
BASOLATERAL MEMBRANE OF INTERCALATED CELLS OF DISTAL TUBULES AND
COLLECTING DUCTS.
ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms-2;
                                    . Gaps
                                                                                                                                                                                                                                                                                                                       Kudrycki K.E., Shull G.E., "Primary structure of the rat kidney band 3 anion exchange protein
                                                                                                                                                                    28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Band 3 anion transport protein (Anion exchange protein 1) (AE 1).
SIC4A1 OR AE1.
                                   ;
            Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00955; HCO3_cotransp; 1.
PIGRFAMs; PR01231; HCO3TRNSPORT.
PIGRFAMs; TGR000834; ae, 1.
PROSTTE: PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: Kidney.
SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
          Score 98; DB 1; 1
Pred. No. 1.5e-08;
Mismatches 0;
                                                                                                                                            927 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Kidney;
IsoId=P23562-2; Sequence=VSP_000455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId-P23562-1; Sequence-Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
                                                                                                                                                                                                                                                                                                                                                 deduced from a cDNA.";
J. Biol. Chem. 264:8185-8192(1989).
                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; J04793; AAA40800.1; ALT_INIT
EMBL; L02943; AAA40801.1; -.
100.0%; Scc.
100.0%; Pre
                                                                      731 SVTHANALTVMGKASTPGAA 750
                                                                                                                                                                                                                                                                                                 TISSUE=Kidney;
MEDLINE=89255254; PubMed=2722777;
                                                         1 SVTHANALTVMGKASTPGAA 20
                                                                                                                                                                 01-NOV-1991 (Rel. 20, Created)
                                                                                                                                                                                                                                                                                       SEQUENCE OF 46-927 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-45 FROM N.A.
                                   Conservative
                                                                                                                                            STANDARD;
                                                                                                                                                                                                                            Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=Erythrocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A33810; A33810.
          Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P02730; 1BTS
                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                            B3AT_RAT
P23562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <del>-</del>
                                                                                                                    RESULT 2
                                                                                                                                  B3AT_RAT
                                                          ò
                                                                               q
```

```
Kopito R.R., Lodish H.F.; "Primary structure and transmembrane orientation of the murine anion exchange protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Band 3 anion transport protein (Anion exchange protein 1) (AE 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. . ) (PROBABLE)
PALMITATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 91; DB 1; Length 927; Pred. No. 2.2e-07;
CYTOPLASMIC (POTENTIAL).
MEMBRANE (ANION EXCHANGE).
POTENTIAL.
POTENTIAL.
                                                                                                                     POTENTIAL.
POTENTIAL.
EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                                                                          POTENTIAL.
EXOPLASMIC LOOP (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARTIAL SEQUENCE FROM N.A.
MEDIINE-87250387; PubMed-3036795;
Kopito R.R., Andersson M., Lodish H.F.;
"Structure and organization of the murine band 3 gene.";
J. Biol. Chem. 262:8035-8040(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Missing (in isoform Kidney) /FTId=VSP_000455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUL-1987) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        681A228474E5E9DE CRC64;
                                                                                                                                                                                             POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-66034211; PubMed-3840489;
Kopito R.R., Lodish H.F.;
"Structure of the murine anion exchange protein.";
J. Cell. Biochem. 29:1-17(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          929 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                               POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                            POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 SVTHANALTVMGKASGPGAA 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=85268011; PubMed=2410791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 11-929 FROM N.A.
MEDLINE=86274622; PubMed=3015590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SVTHANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103172 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.9%;
95.0%;
```

ő

4

```
FT FT S
                                                                                                                                                                                                      a
                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                  after in situ proteolysis.";
Biochim. Biophys. Acta 980:291-298(1989).
-! FUNCTION: BAND 3 IS THE MAJOR INTEGRAL GLYCOPROTEIN OF THE
-! FUNCTION: BAND 3 IS THE MAJOR INTEGRAL GLYCOPROTEIN OF THE
ERYTHROCYTE MEMBRANE. BAND 3 HAS TWO FUNCTIONAL DOMAINS. ITS
INTEGRAL DOMAIN MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS
THE MEMBRANE, WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING
SITES FOR CYTOSKELETAL PROTEINS, GLYCOLYTIC ENZYMES, AND
                                                                                                                                                                                                                                                                                                                   SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY AND APPERARS TO BE TETRAMERIC.
SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                    Major proteolytic fragments of the murine band 3 protein as obtained
                                                                                                                                     Raida M., Wendel J., Kojro E., Fahrenholz F., Fasold H., Legrum B.,
Demuth D.R., Showe L.C., Ballantine M., Palumbo A., Fraser P.J., Cioe L., Rovera G., Curtis P.J.; "Cloning and structural characterization of a human non-erythroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. . .) (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Anion exchange; Erythrocyte; Lipoprotein; Palmitate; Alternative Splicing.
DOMAIN 423 929 MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISOId=P04919-2; Sequence-VSP_000454;
TISSUE SPECIFICITY: ERYTHROCYTE.
SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                     Event-Alternative splicing; Named isoforms-2;
                                                                                                    SEQUENCE OF 33-47; 360-375; 382-395 AND 578-590.
                                                                                                                                                                                                                                                                                                                                                                                                     Name=Erythrocyte;
IsoId=P04919-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:109393; Slc4al.
MGD; MGI:109393; Slc4al.
InterPro; IPR001717; Anion_exchange.
InterPro: IPR003203; HC03_cotranspt.
Pfam; PF00955; HC03_cotranspt.
PRINTS; PR01231; HC03TRNSPORT.
                                                                                                                     MEDLINE=89229233; PubMed=2713407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X02677; CAA26506.1; -. EMBL; M29379; AAA37187.1; -. EMBL; U02756; AAA37278.1; -. EMBL; X09317; CAA27555.1; -. PIR; A25314; A25314;
                                                   band 3-like protein."; EMBO J. 5:1205-1214(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGRFAMS; TIGRO0834; ae; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEN
                                                                                                                                                      Passow
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                     ö
                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nacione (1978) Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kudrycki K.E., Newman P.R., Shull G.E.;
"CDNA cloning and tissue distribution of mRNAs for two proteins that
are related to the band 3 Cl./RCO3-exchanger.";
J. Biol. Chem. 265:462-471(1990).
                                                                                                                                                                                                                                                                                                                                                        01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
SLC4A2 OR AE2 OR B3RP2.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
DOMAIN 1 704 CYTOPLASMIC (POTENTIAL).
DOMAIN 705 1234 MEMBRANE (ANION EXCHANGE).
TRANSMEM 705 728 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kopito R.R.; "Functional expression and subcellular localization of an anion
                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-90319095; Pubmed-2371270;
Lindsey A.E., Schneider K., Simmons D.M., Baron R., Lee B.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exchanger cloned from choroid plexus.";
Proc. Natl. Acad. Sci. U.S.A. 87:5278-5282(1990).
-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
                                                                                                              92.9%; Score 91; DB 1; Length 929; 95.0%; Pred. No. 2.2e-07; tive 0; Mismatches 1; Indels
                     Missing (in isoform Kidney). /FTId=VSP_000454.
                                                          467 G -> S (IN REF. 5).
103135 MW; 5C0E281C394FB614 CRC64;
 PALMITATE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Integral membrane protein. -!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                         PRT; 1234 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A34911; A34911.
HSSP; P02730; 1BTQ.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HC03_cotranspt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90094439; PubMed=2294114;
                                                                                                                                                                                                                              SVTHANALTVMGKASGPGAA 768
                                                                                                                                                                                          1 SVTHANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00955; HCO3_cotransp; 1.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; J05166; AAA40799.1; -.
                                                                                                                                 Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FIGREAMS; TIGRO0834; ae;
                                                                                                                                                                                                                                                                                                                         STANDARD;
861
79
                                                          467
929 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Stomach;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Brain;
                   VARSPLIC
                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                         B3A2_RAT
                                                                                                                  Query Match
                                                          CONFLICT
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
         -!- TISSUE SPECIFICITY: Isoform a is widely expressed at similar levels in all tissues examined. Isoforms bl and b2 are predominantly expressed in stomach although they are also detected at lower levels in other tissues. Isoform c1 is stomach-specific. Isoform c2 is expressed at slightly higher levels in lung and stomach than in other tissues.
-!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PALMITATE (BY SIMILARITY).
MSSAPRRPASGADSLHT -> MDFLLRPQ (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ERTSPSPPTQTPHQEAAPRASKGAQTG -> MPAFQEWKSG
GLREEAVFGAHGCSVCR (in isoform C2).
                                                                                                                                                                                                                                                                                                                       HSSP; P02/34); IDLY.
MGD; MGI:109351; S1c4a2.
MGD; MGI:109351; S1c4a2.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR0013020; HC03_cotranspt.
Pfam; PR001231; HC03_cotransp; 1.
PR01175; PR001231; HC03_RNSPORT.
TIGREAMS; TIGR00834; aa. 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Palmitate; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLY-SER.
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
POTENTIAL.
EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTId=VSP_000461.
A -> G (IN REF. 2).
W; 1A0782C0071782EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
MEMBRANE (ANION EXCHANGE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /FTId=VSP_000457.
MSSAPRRPASGADSLHT -> MTQ
IsoId=P13808-5; Sequence=VSP_000459, VSP_000461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Missing (in isoform C2). /FIId=VSP_000459.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Missing (in isoform C1). /FTId=VSP_000460.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 73; DB 1; Pred. No. 0.00033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /FTId=VSP_000458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIS-RICH.
                                                                                                                                                                                                                                      EMBL, AF255774; AAG23154.1; --
EMBL, AF255774; AAG23155.1; --
EMBL, AF255774; AAG23156.1; --
EMBL, AF255774; AAG23158.1; --
EMBL, AF255774; AAG23157.1; --
PIR; A31789; A31789.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74.58;
83.38;
                                                                                                                                                                                                                           EMBL; J04036; AAA65505.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  914
929
929
929
929
929
931
87
87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
TRÀNSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'ARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
ö
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       B3A2_MOUSE STANDARD; PRT; 1237 AA.
P13808; Q9ES09; Q9ES10; Q9ES11; Q9ES12; Q9ES13;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM A).
MEDLINE-89034212; PubMed-3182834;
Alper S.L., Kopito R.R., Libresco S.M., Lodish H.F.;
"Cloning and characterization of a murine band 3-related cDNA from kidney and from a lymphoid cell line.";
J. Biol. Chem. 263:17092-17099(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY. MEDILINE-20462926, Pubmed-11006093. Lecanda J., Urtasun R., Medina J.F.; "Mojecular cloning and genomic organization of the mouse AE2 anion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                     (POTENTIAL).
                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exchanger gene.";
Biochim. Blophys. Res. Commun. 276:117-124(2000).
-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
DISTRIBUTION.
                                                                                                                                                                                                                                                                                                         Score 73; DB 1; Length 1234;
                                                                                                                                                                      N-LINKED (GLCNAC. . .) (POTE
N-LINKED (GLCNAC. . .) (POTE
N-LINKED (GLCNAC. . .) (POTE
PALMITATE (BY SIMILARITY).
G -> A (IN REF. 2).
RR -> PG (IN REF. 2).
                          POTENTIAL.
EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                                                                                                                                                      M -> I (IN REF. 2).
M -> I (IN REF. 2).
MW; FAB4ED12BB916216 CRC64;
                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Integral membrane protein. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=5;
                                                                                                                                                                                                                                                                                                                       Pred. No. 0.00033;
                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=P13808-3; Sequence=VSP_000457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=P13808-4; Sequence=VSP_000460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=P13808-2; Sequence=VSP_000458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId-P13808-1; Sequence-Displayed;
                                                     POTENTIAL.
                                                                                                       POTENTIAL.
                                                                                                                                  POTENTIAL.
                                                                                          POTENTIAL.
                                                                                                                      POTENTIAL.
                                                                                                                                                PRO-RICH.
                                                                                                                                                            HIS-RICH.
                                                                                                                                                                                                                                                                                                                                                                            1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                           74.5%;
                                                                                                                                                                                                                                                                                136635
                                                                                                                                                                                                                                                                                                                                     15; Conservative
                                                                                          1003
1050
1129
1192
                                                                                                                                                                                                                                                                  1156 115
1234 AA;
                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                       1029
1084
1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLC4A2 OR AE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=B2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=B1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=C2;
                                     DOMAIN
TRANSMEM
                                                                DOMAIN
TRANSMEM
                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                  TRANSMEM
                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                  SEQUENCE
                          PRANSMEM
                                                                                          LRANSMEN
                                                                                                       TRANSMEN
                                                                                                                      FRANSMEN
                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                LIPID
                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       å
                                                                                                                                                                                                                                                                                                                                                                                        g
```

(in isoform B1).

(POTENTIAL). (POTENTIAL).

ø

```
1237 AA;
                                                                                                                                                                                                                                                                                                                                                            DISTRIBUTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1033
1088
1160
                                                                                                                                                                                                             SLC4A2 OR AEZ
                                                                                                                                      B3A2_CAVPO
 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RANSMEN
                                                                                                                                                 092058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                            B3A2_CAVPO
                                                                                                                   RESULT 7
                                                                                  qq
                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeleb-sib.ch).
 ö
 Gaps
                                                                                                              01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
SLC4A2 OR AE2.
                                                                                                                                                                   Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ransmembrane; Glycoprotein; Transport; Antiport; Ion transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . .) (POTENTIAL). . . . (POTENTIAL). . . . (POTENTIAL). . .
                                                                                                                                                                                                                                 STRAIN=New Zealand white;
MEDLINE=93035730; PubMed=1415547;
Chow A., Dobbins J.W. Aconson P.S., Igarashi P.;
"CDNA cloning and localization of a band 3-related protein from
 ;
0
                                                                                                                                                                                                                                                                                     Am. J. Physiol. 263:G345-G352(1992).
-I- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
DISTRIBUTION:
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (PCN-LINKED (GLCNAC. . .) (PCN-LINKED (GLCNAC. . .) (PCN-LINKED (GLCNAC. . .) (PCN-LINKED (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEMBRANE (ANION EXCHANGE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL)
 3;
                                                                                           1237 AA.
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP, P02730; IBTQ.
InterPro; IPR001312; Anton_exchange.
InterPro; IPR001302; HC03_cotranspt.
Pfam; PP00955; HC03_cotranspt.
PRINTS; PR01231; HC03TRNSPORT.
TIGRAMS; TIGROMS31, as; 1.
TIGRAMS; TIGROMS31, as; 1.
PROSITE; PS00139; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Palmitate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                              SVTHANALTVMSKAVAPG 1074
0;
                   SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; S45791; AAB23488.1; -. PIR; A56764; A56764.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anion exchange; Lipoprotein;
Conservative
                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1006
1053
1132
1195
316
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                   NCBI_TaxID=9986;
15;
                                                                                             B3A2_RABIT
                                        1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRANSMEM
                                                                                                                                                                                                                                                                            ileum."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NI WWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIPID,
Matches
                                        g
                                                                                             ð
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-NHH 2; TISSUE-Organ of Corti;
MEDLINE-99023787; PubMed-9804866;
Mhatre A.N., Charachon G., Alper A.L., Lalwani A.K.;
"The guinea pig cochlear A2 anion exchanger: cDNA cloning and in situ localization within the cochlea.";
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                             16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (AE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Cavildae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochim. Biophys. Acta 1414:1-15(1998).
                                         Length 1237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXOPLASMIC LOOP (POTENTIAL).
                                                                                          Indels
136535 MW; 2811D11051552BB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
MEMBRANE (ANION EXCHANGE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL)
                          Score 73; DB 1; Ler
Pred. No. 0.00033;
                                                                                                                                                                                                                                                                                                      PRT; 1238 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRO-RICH.
HIS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interPro; IPR001117; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfant; PF00955; HCO3_cotranspt. 1.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                1057 SVTHANALTVMSKAVAPG 1074
                                                                                       0;
                                                                                                                                      18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF121253; AAD19700.1; -
                                              74.5%;
83.3%;
                                                                                                                                        1 SVTHANALTVMGKASTPG
                                                                                            Conservative
                                                                                                                                                                                                                                                                                                         STANDARD;
                                           Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1BTO
                                                                                                                                                                                                                                                                                                                                                                                                                                             anion exchanger).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10141;
```

```
Name=B1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
    SOLUTION DE LA CONTROL DE LA C
                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               **REDLINE=22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Carainci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Robards P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mitching M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Ablakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Ablakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Ablakesley R.W., Touchman J.W., Marra M.A., Skalska U., Smailus D.E., Generation and initial analysis of more than 15,000 full-length human and mouse colls Sequences."
                                                                                                                                                                                                                                                                                                                                                               B3A2_HUMAN STANDARD; PRT; 1241 AA. P04920; 09691.3; 13-404-1987 (Rel. 05, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 42, Last annotation update) Anion exchange protein 2 (Non-erythroid band 3-like protein) (BND3L). SLC4A2 OR AEZ OR EPB3L1 OR HKB3 OR MPB3L.
                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 375-1241 FROM N.A.
MEDIINE-86274622; PubMed-3015590;
MEDIINE-86274622; PubMed-3015590;
Demuth D.R., Showe L.C., Ballantine M., Palumbo A., Fraser P.J.,
Cioe L., Rovera G., Curtis P.J.;
"Cloning and structural characterization of a human non-erythroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi;
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
PALMITATE (BY SIMILARITY).
MW; FA1739862ED5ADBF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM A).
MEDLINE-92223115; PubMed-1562608;
Gehrig H., Mueller W., Appelhans H.;
"Complete nucleotide sequence of band 3 related anion transport
                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
                                                                                                                            Length 1238;
                                                                                                                              Db 1,
. 0.00033;
. 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Integral membrane protein. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein AE2 from human kidney.";
Biochim. Biophys. Acta 1130:326-328(1992)
                                                                                                                              Score 73;
Pred. No. (
                                                                                                                                                                                                                                       1058 SVTHANALTVMSKAVAPG 1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM B1).
                                                                                                                                                                                                                 1 SVTHANALTVMGKASTPG 18
856 856
865 865
879 879
1170 · 1170
1238 AA; 137358 M
                                                                                                                            74.5%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           band 3-like protein.";
EMBO J. 5:1205-1214(1986)
                                                                                                                                                Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISTRIBUTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain
CARBOHYD
CARBOHYD
CARBOHYD
LIPID
                                                                                    SEQUENCE
                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                           B3A2_HUMAN
                                                                                                                                                                                                                                                                                                                         RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                         g
```

```
between the Swiss Institute of Bloinformatics and the EMBL outstation-
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L -> V (IN REF. 1).
LLGHHGGGAESDPHVTEPLMGGVPE -> CWGITMVRGLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EL -> DV (IN REF. 1 AND 3).
AAGAAEDDPLRRTGRP -> RQGQLKMIPSADGAA (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Palmitate; Alternative splicing.
CYTOPLASMIC (POTENTIAL).
MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
POTENTIAL.
POTENTIAL.
EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REF. 1 AND 3).
Q -> R (IN REF. 1 AND 3).
L -> P (IN REF. 1 AND 3).
WW; B116908C5A71DB77 CRC64;
                                 IsoId-P04920-2; Sequence=VSP_000456; SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PALMITATE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTPTSPSLSWEVFLR (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                           MIM; 109280; -. Geombrane fraction; TAS. 60; 60:0005624; C:membrane fraction; TAS. 60; 60:0008509; F:anion transporter activity; TAS. 60; 60:0006820; P:anion transport; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
IsoId=P04920-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotranspt.
TIGRNO955; HCO3TRNSPORT.
TIGROBAS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRO-RICH.
                                                                                                                                                                                                                                           EMBL, X62137; CAA44067.1; -. BMBL, BC009386.3; -. EMBL, BC009434; AAH099386.1; -. EMBL, X03918; CAA27556.1; -. PITS, S21086; S21086. HSSP, P02730; 1BTO. Genew, HGNC:11028; SLC4A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anion exchange; Lipoprotein;
DOMAIN 1 707
DOMAIN 708 1241
TRANSMEM 737 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        816
8477
933
933
1010
11136
11136
11199
859
888
888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68
74
92
122
157
157
399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              486
681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      824
902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    824 82
902 90
1241 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
```

ω

```
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
TRANSMEM
                                                                              Query Match
                                            CARBOHYD
                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRANSMEM
                                                                                                                                                                                   RESULT 10
B3AT_ONCMY
                                                                                                    Matches
                                                                                                                                                                                                            FT
                                                                                                                           δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                     ö
                                                                                                                                                                                                                                                             MEDLINE-89039870; PubMed=318555;
MEDLINE-89039870; PubMed=318555;
Mim H. N.C., Yew N.S., Ansorge W.D.;
Vennstroem B., Zenke M., Engel J.D.;
"Two different mRNAs are transcribed from a single genomic locus encoding the chicken erythrocyte anion transport proteins (band 3).";
Mol. Cell. Biol. 8:4416-4424(1988).
-!-FUNCTION: BAND 3 IS THE MAJOR INTEGRAL GLYCOPROTEIN OF THE ERYTHROCYTE MEMBRANE. BAND 3 HAS TWO FUNCTIONAL DOMAINS. ITS INTEGRAL DOMAIN MEDIATES A 1:1 EXPHANGE OF INORGANIC ANIONS ACROSS INTEGRAL DOMAIN MEDIATES A 1:1 EXPHANGE OF INORGANIC ANIONS ACROSS
                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY
                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                               THE MEMBRANE, WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING SITES FOR CYTOSKELETAL PROTEINS, GLYCOLYTIC ENZYMES, AND
                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGRRAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Anion exchange; Erythrocyte.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXOPLASMIC LOOP (POTENTIAL).
POTENTIAL.
POTENTIAL.
                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                            AND APPEARS TO BE TETRAMERIC. SUBCELLULAR LOCATION: Integral membrane protein. SITSSUE SPECIFICITY: ERYTHROCYTE. SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL) POTENTIAL.
Pred. No. 0.00033;
                                                                                                                                             01-APR 1990 (Rel. 14, Created)
01-ARR-1990 (Rel. 14, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
and 3 anion transport protein.
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotransp; 1.
PRINYS; PR01231; HCO3TRNSPORT.
                                                       1061 SVTHANALTVMSKAVAPG 1078
                    ;
0
                                          1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M23404; AAA48753.1; -.
         83.3%;
        Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          922
4437
4699
492
523
554
5579
614
6611
730
                                                                                                                                                                                                                                          NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                       HEMOGLOBIN.
                                                                                                                        B3AT_CHICK
P15575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                               g
                                                                                                                         à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem. J. 285:17-23(1992).

-I- FUNCTION: BAND 3 HAS TWO FUNCTIONAL DOMAINS: ITS INTEGRAL DOMAIN MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS THE MEMBRANE, WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING SITES FOR CYTOSKELETAL AND OTHER PROFIEINS (BY SIMILARITY).

-I- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY AND APPEARS TO BE TETRAMERIC (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane; Glycoprotein; Anion exchange; Lipoprotein; Palmitate. DOMAIN 1 392 (YTOPLASNIC (POTENTIAL). DOMAIN 393 918 MEMBRANE (ANION EXCHANGE). TRANSMEM 393 413 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID=8022;
791 POTENTIAL.
817 POTENTIAL.
876 POTENTIAL.
876 N-LINKED (GLCNAC. . ) (PROBABLE).
102223 MW; FF4ECAD6D60CF0CF CRC64:
                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                               Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hubner S., Michel F., Rudloff V., Appelhans H.; "Amino acid sequence of band-3 protein from rainbow trout erythrocytes derived from cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL. EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                            Score 71; DB 1; Pred. No. 0.00052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 27, Created)
(Rel. 33, Last sequence update)
(Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         918 AA.
                                                                                                                                                                                                                                     5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INCEFFIG. ALANCESCY, TEACHER PERSONS 1. PROBASS; HC03-cotransp; 1. TIGREAMS; TIGRO0834; ae; 1. PROSITE; PS00219; ANION_EXCHANGER_1; 1. PROSITE; PS00220; ANION_EXCHANGER_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4SSP; P02730; 1BTQ.
InterPro; IPR001717; Anion_exchange.
interPro; IPR003209; HCO3_cotranspt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92344566; PubMed=1637296;
                                                                                                                                                                                                                                                                                                                                01-0cT-1993 (Rel. 27, Created)
01-FFB-1996 (Rel. 33, Last sequ
15-JUL-1999 (Rel. 38, Last and
Band 3 anion exchange protein.
SLC4A1 OR AE1.
                                                                                                                                                                                                                                                                                               1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                            72.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X61699; CAA43868.1; -.
                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S24318; S24318.
   774
796
855
653
922 AA;
                                                                                                                                                                                                       Local Similarity
Les 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B3AT_ONCMY
```

```
PIR; A33638; A33638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B3A3_RAT
P23348;
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                           VARSPLIC
                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                       VARSPLIC
                                                                                                                                                                                                                                                                                                                                                            VARSPLIC
                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                     VARSPLIC
                                                                                                                                                                TRANSMEM
                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                           DOMAIN
                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
                                                                                                                                                                                                                                                                                                                                                                      FFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                              ö
                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-90075236; Pubmed-2686841;
Kopito R.R., Lee B.S., Simmons D.M., Lindsey A.E., Morgans C.W.,
                                                                       POTENTIAL.
PALMITATE (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Morgans C.W., Kopito R.R.; "Generation of truncated brain AE3 isoforms by alternate mRNA processing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                 "Regulation of intracellular pH by a neuronal homolog of the erythrocyte anion exchanger."; Cell 59:927-937(1989).
                                                                                                                                     Score 63; DB 1; Length 918;
Pred. No. 0.012;
); Mismatches 4; Indels
           POTENTIAL.
EXOPLASMIC LOOP (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                          01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 3 (Neuronal band 3-like protein).
SLC4A3 OR AE3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=P16283-3; Sequence=VSP_000466, VSP_000467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- TISSUE SPECIFICITY: NEURONAL.
-i- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId-P16283-2; Sequence-VSP_000464, VSP_000465;
  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5. Cell Sci. 106:1275-1282(1993).
-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event-Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING MEDLINE-94171936; Pubmed-8126106;
                                                                                                                                                                                                                                                             PRT; 1227 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=P16283-1; Sequence=Displayed;
                                                    POTENTIAL. POTENTIAL.
                                           POTENTIAL
                                                                                                                     MM.
                                                                                                                                                              ö
                                                                                                                                                                                               744 SVTHANALTVMSKGPKP 760
                                                                                                                                                                                   1 SVTHANALTVMGKASTP 17
                                                                                                                                        64.3%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M28383; AAA37184.1; -. EMBL; S69314; AAB30140.1; -.
                                                                                                                     101893
                                                                                                                                                              13; Conservative
                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
                                                                                                                    918 AA;
                                                                                                                                                    Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=311-AE3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=14-AE3;
 602
617
638
674
712
772
772
794
853
853
852
546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=FL-AE3
                                                                                                                                                                                                                                                                                                                                                                                                                          Schneider K.;
                                                                                                                                                                                                                                                           B3A3_MOUSE
DOMAIN
TRANSMEM
DOMAIN
                                                    TRANSMEM
TRANSMEM
                                                                          TRANSMEM
                                                                                               CARBOHYD
                                                                                                                     SEQUENCE
                                                                                                                                          Query Match
                               TRANSMEM
                                                                                                         CARBOHYD
                                           TRANSMEM
                                                                                                                                                                                                                                                                      P16283
                                                                                                                                                                                                                                       RESULT 11
B3A3_MOUSE
                                                                                      LIPID
                                                                                                                                                             Matches
                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                       FT FT FT FT S
                                                                                                                                                                                   δ
```

```
/FTIG-VSP_000464.
Missing (in isoform 311-AE3).
/FTIG-VSP_000465.
KPLHMPGGDGHRGKSLK -> FCVLRSPSPCLGETVTEGKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-9009439; PubMed-2294114;
MEDLINE-9009439; PubMed-2294114;
Kudrycik K.E., Newman P.R., Shull G.E.;
"CDNA cloning and tissue distribution of mRNAs for two proteins that are related to the band 3 cl-/HCO3-exchanger.";
J. Biol. Chem. 265:462-471(1990).
-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PALMITATE (BY SIMILARITY).
AALLDLEQTTL -> RAFWAGNESLL (in isoform
                                                                                                            N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 61; DB 1; Length 1227; Pred. No. 0.034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (in isoform 14 AE3).
/FTId=VSP 000466.
Missing (in isoform 14-AE3).
/FTId=VSP 000467.
MW; D5BEC46E03F4251C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 3 (Neuronal band 3-like protein).
SLC4A3 OR AE3 OR B3RP3.
                                                                                                                                                                                                              CYTOPLASMIC.
MEMBRANE (ANION EXCHANGE)
POTENTIAL.
                                                                                                                                                                                                                                                                                                                               POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1227 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-GLU.
HSSP; P02730; 1BTQ.
MGD; MGI:109350; S1c443.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                311-AE3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1048 SVTHVNALTVMRTAIAPG 1065
                                                                      Pfam; PF00955; HC03_cotransp; 1. PRINTS; PR01231; HC03TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1227 AA; 135164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 62.2%;
Best Local Similarity 72.2%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145
868
1160
391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1227
                                                                                                                                                                                                                                   1227
                                                                                                                                                                                                                                                   730
773
815
846
905
920
941
997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          503
                                                                                                                                                                                                                                                                                                                                                                                                                           1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          487
```

ö

```
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
 between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                      ö
          This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 3 (Neuronal band 3-like protein) (Cardiac/brain band 3-like protein) (CAE3/BAE3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                    PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
Anion exchange; Lipoprotein; Palmitate.
DOMAIN | CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL). PALMITATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yannoukakos D., Stuart-Tilley A., Fernandez H., Fey P., Duyk G., Alper, S.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 1227;
                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
                                                                                                                                                                                                                                                                                                                                                                                 3EB1620EE011730E CRC64;
                                                                                                                                                                                          CYTOPLASMIC.
MEMBRANE (ANION EXCHANGE)
                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                            0.034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1232 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                    POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                     Score 61;
                                                                                                                                                                                                                                                               POTENTIAL. POTENTIAL.
                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                POLY-SER.
POLY-LEU.
                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                                                                                                                                           N-LINKED
                                                                                                        Interpro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotransp; 1.
PRINTS; PR01231; HCO3TRNSPORT.
TIGRFAMS; TIGR00834; ae; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM BAE3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Heart;
MEDLINE=95008042; PubMed=7923606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                |||| ||||||| || ||| SVTHVNALTVMRTAIAPG 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SVTHANALTVMGKASTPG 18
                                                                              EMBL; J05167; AAA40798.1; -. PIR; B34911; B34911.
                                                                                                                                                                                                                                                                                                                                                                                                    62.2%;
72.2%;
                                                                                                                                                                                                                                                                                                                                                                       1179 1182
1227 AA; 135406
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 62.2
Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                        1123
1186
868
                                                                                                                                                                                                                                                                                                                     1160
                                                                                                                                                                                                                                                                        997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
                                                                                                  HSSP; P02730; 1BTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                              155
307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B3A3_HUMAN
P48751;
                                                                                                                                                                                                 DOMAIN
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                           CARBOHYD
LIPID
                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1048
                                                                                                                                                                                                                                                                PRANSMEM
                                                                                                                                                                                                                            PRANSMEM
                                                                                                                                                                                                                                                                                          FRANSMEM
                                                                                                                                                                                                                                                                                                    FRANSMEM
                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                         EXCHANGE IN CARDIAC MYOCYTES. BOTH BAE3 AND CAE3 FORMS TRANSPORT
"Molecular cloning, expression, and chromosomal localization of two isoforms of the AE3 anion exchanger from human heart."; Circ. Res. 75:603-614(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSoId=P48751-2; Sequence=VSP_000462, VSP_000463;
-!- TISSUE SPECIFICITY: BOTH BAE3 AND CAE3 ARE EXPRESSED IN FAILING
                                                                                                                                                         TISSUE-Heart;
Kudo S., Mattei M.-G., Bloor C.M., Fukuda M., Ranney H.M., Xu A.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
DISTRIBUTION. MEDIATES AT LEAST A PART OF THE CL(-)/HCO3(-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PFUUJU; HC03TKW3. ...
TIGREMS; TIGRO0834; ae; 1.
TIGREMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; Alternative splicing.
"...hrane; Glycoprotein; Palmitate; Alternative splicing."...hranesMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIM; 106195; -.
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0005624; C:integral to plasma membrane; TAS.
GO; GO:0005622; C:incorganic anion exchanger activity; TAS.
GO; GO:0006832; P:small molecule transport; TAS.
InterPro; IPR001317; Anion_exchange.
InterPro; IPR001317; Anion_exchange.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PALMITATE (BY SIMILARITY)
Missing (in isoform CAE3)
/FTId-VSP_000462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -! - SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=P48751-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-GLU.
PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-SER.
POLY-LYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLY-LEU
                                                                                                                               SEQUENCE FROM N.A. (ISOFORM CAE3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U05596; AAA50748.1; -.
EMBL; L27213; AAB05850.1; -.
PIR; I38496; I38496.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P02730; 1BTQ.
Genew; HGNC:11029; SLC4A3.
MIM; 106195; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         946
1002
1049
1128
1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=BAE3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VENTRICLE
```

```
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haemophilus influenzae.
                                                                                                                                                                                                                                                                        446
1188
                                                                    926
947
1003
1050
1129
1192
874
                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y003_HAEIN
                                                                                                      TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                         CARBOHYD
                                                      TRANSMEM
                                                                                        TRANSMEM
                                                                                                                                       TRANSMEM
                                                                                                                                                           TRANSMEM
                                      TRANSMEM
                     FRANSMEN
                                                                                                                                                                                                          DOMAIN
                                                                    DOMAIN
                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
Y003_HAEIN
                                                                                                                                                                                         LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane; Glycoprotein; Transport; Antiport; Ion transport; Anion exchange; Lipoprotein; Palmitate.

OMAIN 1 709 CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 3 (Neuronal band 3-like protein) (Anion SIC4Aa OR AE3.
                                                                                                                                                                                                                                                                                                                                           ;
/FTId=VSP_000463.

I -> V (IN REF. 2).
R -> P (IN REF. 2).
P -> S (IN REF. 2).
S -> G (IN REF. 2).
D -> A (IN REF. 2).
GS -> FI (IN REF. 2).
F -> L (IN REF. 2).
F -> L (IN REF. 2).
GSLA -> D (IN REF. 2).
GSLA -> D (IN REF. 2).
S -> C (IN REF. 2).
S -> C (IN REF. 2).
C -> P (IN REF. 2).
                                                                                                                                                                                                                                                                                                        Score 61; DB 1; Length 1232;
Pred. No. 0.034;
0; Mismatches 5; Indels
   SPS -> MPA (in isoform CAE3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Kidney;
Abuladze N., Pushkin A., Kurtz I.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEMBRANE (ANION EXCHANGE) POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- TISSUE SPECIFICITY: NEURONĂL.
-i- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -! - SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP, P02730; 1BTQ.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfam; PP00955; HCO3_cotranspt.
PRINTS; PR01231; HCO3TRNSPORT.
TIGREAMS; TIGROB34; ae. 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                1053 SVTHVNALTVMRTAIAPG 1070
                                                                                                                                                                                                                                                                          1232 AA; 135706 MW;
                                                                                                                                                                                                                                                                                                                                                                           1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF031650; AAB86859.1; -.
                                                                                                                                                                                                                                                                                                          62.2%;
72.2%;
                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 72.2
Matches 13; Conservative
                                                                                                                        813
822
861
861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9986;
                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
TRANSMEM
                                   CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                       CONFLICT
                                                                                                                                                      CONFLICT
   VARSPLIC
                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                       CONFLICT
   ò
                                                                                                                                                                                                                                                                                                                                                                                                             g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTIFICATION BY MASS SPECTROMETRY.
MEDLINE-2013/488; Pubmed=10675023;
Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B.,
Gray C., Fountoulakis M.;
"Two-dimensional map of the proteome of Haemophilus influenzae.";
Electrophoresis 21:411-429(2000).
-!- SIMILARITY: BELONGS TO THE COF/YBHA/YIDA/YIGL (E.COLI) / YCSE/YXEH·
(B.SUBTILIS) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95350630; PubMed=7542800; Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Felischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Karlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL).
PALMITATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 61; DB 1; Length 1233; Pred. No. 0.034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AE486423E9818583 CRC64;
                                                      POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
208-FEB-2003 (Rel. 41, Last annotation update)
Protein H10003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                 POTENTIAL. POTENTIAL.
                         POTENTIAL.
                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                              POTENTIAL.
POTENTIAL
                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                         HIS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                      POLY-SER
                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-LYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1054 SVTHVNALTVMRTAIAPG 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
Μ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.2%;
72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SVTHANALTVMGKASTPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 72.2'
```

```
0;
entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 50.0%; Score 49; DB 1; Length 262; Best Local Similarity 55.6%; Pred. No. 0.73; Matches 10; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                   REMEL, U32686; AAC21682.1; -.
RIGR; H64139; 164139.
TIGR; H10003; -.
RITCEPTO; IPRO06379; HAD_SF_IIB.
RITCEPTO; IPRO01584; Hydrolase.
RITCEPTO; IPRO0150; Hypothet_cof.
R PAGM, PF00702; Hydrolase.
R TIGREAMS; TIGRO1484; HAD-SF-IIB; I.
R TIGREAMS; TIGRO1484; HAD-SF-IIB; I.
R PROSITE; PS01228; COF_1; I.
R PROSITE; PS01229; COF_2; I.
COMPLETE PS01229; COF_2; I.
SEQUENCE 262 AA; 29353 MW; ZE9657AC4F2093DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :||| | || |::| |:|
175 SHANFLEVMHKSATKGSA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 THANALTVMGKASTPGAA 20
SO NEW TON THE TON TON THE TON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
```

Search completed: September 3, 2003, 11:46:56 Job time : 10.25 secs

Q

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

September 3, 2003, 11:25:42; Search time 9.25 Seconds
(without alignments)
101.679 Million cell updates/sec Run on:

US-10-087-464-3 96 1 GRASTPGAAAQIQEVKEQRI 20 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched: 127863

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ption	homo sapien	rattus norv	mus musculu	gallus gall		mus musculu	oryctolagus	cavia porce	homo sapien	mus musculu	rattus norv	homo sapien	oryctolagus	mumps virus	mumps virus	mus musculu	rattus norv	homo sapien	arabidopsis	escherichia	schizosacch	saccharomyc	haemonchus	rattus norv	arabidopsis	drosophila	human papil	homo sapien	mus musculu	lactococcus	dictyosteli	homo sapien	o cohoriopia
		Description	P02730	P23562	P04919	P15575	P23347	P13808	P48746	09z0s8	P04920	P16283	P23348	P48751	018917	P16072	P16595	002819	063083	002818	P57691	P38055	013923	P53890	P16252	005175	P31168	P54360	081999	P09327	062468	09x764	P08799	P02549	07000
		1																																	
KLES		1	IAN		SE	CK		SE	LI	PO	IAN	SE		IAN	II	PE	PM	SE		AN	TH	LI	Ю	ST	00		TH	ME	2	. NA	SE	υ υ	DI	AN	H.H.
SUMMAKIES		ai .	B3AT_HUMAN	B3AT_RAT	B3AT_MOUSE	B3AT_CHICK	B3A2_RAT	B3A2_MOUSE	B3A2_RABIT	B3A2_CAVPO	B3A2_HUMAN	B3A3_MOUSE	B3A3_RAT	B3A3_HUMAN	B3A3_RABIT	RRPP_MUMPE	RRPP_MUMPM	NCB1_MOUSE	NCB1_RAT	NCB1_HUMAN	RLOC_ARATH	YDJE_ECOLI	CORO_SCHPO	YNQ6_YEAST	CAC2_HAECO	BASP_RAT	DH47_ARATH	FOJO_DROME	VE1_HPV72	VIL1_HUMAN	VIL1_MOUSE	IF2_LACLC		SPCA_HUMAN	T TODA GOOD
		<u>B</u>	7	Н	1	-4	-	Ч	Н	~	~	-4			1	 1		Н	-	Н	-4	Н	-	Н	-	-	Н	Н	Н	Н	-	Н	Н	, ,	-
		Length	911	927	929	922	1234	1237	1237	1238	1241	1227	1227	1232	1233	391	391	459	459	461	323	452	601	448	210	219	265	583	650	826	826	920	2116	2418	005
æ		Match	100.0	2	92.7	63.5	60.4	60.4	60.4	60.4	60.4	56.2	56.2	56.2		•		45.8	45.8	45.8	44.8	44.8	44.8	43.8	42.7	42.7	42.7	42.7	42.7	42.7	42.7	42.7	42.7	42.7	72
		Score	96	83	89	61	28	28	28	58	58	54	54	54	54	45	45	44	44	44	43	43	43	42	41	41	41	41	41	41	41	41	41	41	۲ د
	Result	. No. :	1	7	m	4	ហ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

P40862 salmonella P97350 mus musculu	Q8ylj5 anabaena sp P13434 saccharomyc	_		_	Q9z9c8 chlamydia p		=	Q01649 saccharomyc	_
PROP_SALTY PKP1_MOUSE	RL7_ANASP HAP3_YEAST	RK12_TOBAC	BCHN_CHLAU	PRS4_ORYSA	RADA_CHLPN	DNAA_PROS9	ATPA_MYCPN	CIK1_YEAST	UL93_HCMVA
нн		Н		Н	_	П	П	H	1
500 728	129	186	444	448	453	463	518	594	594
42.2	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7
40.5	40 40	. 40	40	40	40	40	40	40	40
34 35	36 37	38	39	40	41	42	43	44	45

ALIGNMENTS

Wed

PHOSPHORYLATION OF TYR-8; TYR-21; TYR-359 AND TYR-904.
MEDLINE=20400020; PubMed=10942405;
Brunati A.M., Bordin L., Clari G., James P., Quadroni M., Baritono E., Pinna L.A., Donella-Deana A.;
"Sequential phosphorylation of protein band 3 by Syk and Lyn tyrosine Kinases in intact human erythrocytes: identification of primary and secondary phosphorylation sites.";
Blood 96:1550-1557(2000). Z. Yannoukakos D., Vasseur C., Driancourt C., Blouquit Y., Delauney J.,
Wajcman H., Bursaux E.; VARIANT HE 400-ALA--ALA-408 DEL, AND VARIANT MEMPHIS GLU-56.
MEDLINE-92107882; PubMed=1722314;
Jarolim P., Palek J., Amato D., Hassan K., Sapak P., Nurse G.T.,
Kubin H.L., Zhai S., Sahr K.E., Liu S.-C.;
"Deletion in erythrocyte band 3 gene in malaria-resistant Southeast
Asian ovalocytosis."; conformation and a possible molecular mechanism for anion VARÍANT HE 400-ALA--ALA-408 DEL.
MEDLINE-92167271; PubMed=1538405;
Schoffield A.E., Tanner M.J.A., Pinder J.C., Clough B., Bayley P.M.,
Nash G.B., Dluzewski A.R., Reardon D.M., Cox T.M., Wilson R.J.M.,
Gratzer W.B.,
"Basis of unique red cell membrane properties in hereditary ROLE OF GLU-681, AND SEQUENCE OF 665-688.
MEDLINE-92332495; PubMed=1352774;
Jennings M.L., Smith J.S.;
Janings M.L., Smith J.S.;
Janings M.L., Smith B.S.;
Janion-proton cotransport through the human red blood cell band 3 protein. Role of glutemate 681.;
J. Biol. Chem. 267:13964-13971(1992). Cohen C.M.; and y tuccaloosa: Pro-327-->Arg substitution in the cytoplasmic domain of erythrocyte band 3 protein associated with spherocytic hemolytic anemia and partial deficiency of protein 4.2."; Blood 80:523-529(1992). Kawano Y., Okubo K., Tokunaga F., Miyata T., Iwanaga S., Hamasaki Localization of the pyridoxal phosphate binding site at the COOH-terminal region of erythrocyte band 3 protein."; J. Biol. Chem. 263:8232-8238(1988). Hamasaki MEDLINE=91358422; Pubmed=1885574;

MEDLINE=91358422; Pubmed=1885574;

Okubo K., Hamasaki N., Hara K., Kageura M.;

Palmitoylation of cysteine 69 from the COOH-terminal of band 3
protein in the human erythrocyte membrane. Acylation occurs in the middle of the consensus sequence of F-I-IICLAVL found in band 3
protein and G2 protein of Rift Valley fever virus.";

Elol. Chem. 266:16420-16424(1991). ρλ "Human erythrocyte band 3 polymorphism (band 3 Memphis): characterization of the structural modification (Lys 56-->Glu) MEDLINE-92329950; Pubmed-1378323; Jarolim P., Palek J., Rubin H.L., Prchal J.T., Korsgren C., Natl. Acad. Sci. U.S.A. 88:11022-11026(1991) MEDLINE=91329825; PubMed=1678289; MEDLINE-88228050; PubMed-3372523; MEDLINE=93343855; PubMed=8343110; Mol. Biol. 223:949-958(1992) Biochem. J. 213:577-586(1983). protein chemistry methods."; Blood 78:1117-1120(1991). PALMITOYLATION OF CYS-843. VARIANT MEMPHIS GLU-56. OF 834-911 VARIANT HS ARG-327. LEU-868. ovalocytosis."; VARIANT HS SEQUENCE sedneuce, exchange 101

MEDLINE-95134893; PubMed=7530501; Jaroline P., Rubin H.L., Brabbec V., Chrobak L., Zolotarev A.S., Alper S.L., Brugnara C., Wichterle H., Palek J.; Mutations of conserved arginines in the membrane domain of erythroid band 3 lead to a decrease in membrane-associated band 3 and to the phenotype of hereditary spherocytosis."; Blood 85:634-640(1995). "Human erythrocyte protein 4.2 deficiency associated with hemolytic anemia and a homozygous 40 glutamic acid-->lysine substitution in the cytoplasmic domain of band 3 (band 3Montefiore)."; Blood 81:2155-2165(1993). Σ. Bruce L.J., Anstee D.J., Spring F.A., Tanner M.J.; "Band 3 Memphis variant II. Altered stilbene disulfonate binding and the Digo (Dia) blood group antigen are associated with the human erythrocyte band 3 mutation Pro-854-->Leu."; J. Biol. Chem. 269:16155-16158(1994). Bruce L.J., Kay M.M., Lawrence C., Tanner M.J.; "Band 3 HT, a human red-cell variant associated with acanthocytosis and increased anion transport, carries the mutation Pro-868-->Leu in the membrane domain of band 3."; Biochem. J. 293:317-320(1993). VARIANT HS ASP-771.

MEDLINE=96136073; PubMed-8547122;

Maillet P., Vallier A., Reinhart W.H., Wyss E.J., Ott P., Texier P.,

Baillotti F., Tanner M.J., Delaunay J., Alloisio N.;

"Band 3 Chur: a variant associated with band 3-deficient hereditary spherocytosis and substitution in a highly conserved position of Bozon "Changes in the blood group Wright antigens are associated with a mutation at amino acid 658 in human erythrocyte band 3: a site of interaction between band 3 and glycophorin A under certain VARÍANTS HS LYS-40; CYS-518 AND MET-663 DEL.
MEDLINE-96225450; PubMed-8640229;
Eber S.W., Gonzalez J.W., Lux M.L., Scarpa A.L., Tse W.T.,
Dornwell M., Herbers J., Kugler W., Oezcan R., Pekrun A.,
Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;
"Ankyrin-1 mutations are a major cause of dominant and recessive hereditary spherocytosis." VARIANTS HS SER-147 AND MET-488. MEDILINE-97351102; PubMed-9207478; Alloisio M.L., Morle L., Bozon Bursaux E., Maillet P., Goncalves P., Tanner M.J., Tamagnini G., "Characterization of 13 novel band 3 gene defects in hereditary spherocytosis with band 3 deficiency."; Blood 88:4366-4374(1996). Jarolim P., Murray J.L., Rubin H.L., Taylor W.M., Prchal J.T., Ballas S.K., Snyder L.M., Chrobak L., Melrose W.D., Brabec V., MEDLINE-93229758; PubMed-8471774; Rybicki A.C., Qiu J.J.H., Musto S., Rosen N.L., Nagel R.L., Schwartz R.S.; Bruce L.J., Ring S.M., Anstee D.J., Reid M.E., Wilkinson S. VARIANTS HS ASP-285; GLU-455; PRO-707; PRO-834 AND MET-837 VARIANTS HS GLN-760; TRP-760; CYS-808 AND TRP-870. VARIANT BLOOD GROUP DI(A)/MEMPHIS-II. MEDLINE=94266802; PubMed=8206915; Br. J. Haematol. 91:804-810(1995). [21] MEDLINE=97099297; PubMed=8943874; VARIANT BLOOD GROUP WR(A). MEDLINE=95111140; PubMed=7812009; 13:214-218(1996). VARIANT MONTEFIORE LYS-40 Blood 85:541-547(1995). transmembrane segment Fanner M.J.; Genet. conditions. Palek 16]

```
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kudrycki K.E., Shull G.E.;
Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: BAND 3 HAS TWO FUNCTIONAL DOWAINS: ITS INTEGRAL DOWAIN
MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS THE MEMBRANE,
WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING SITES FOR
CYTOSKELETAL AND OTHER PROFIEINS (BY SIMILARITY).
-!- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASOLATERAL MEMBRANE OF INTERCALATED CELLS OF DISTAL TUBULES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kudrycki K.E., Shull G.E.; ^{\circ} "Primary structure of the rat kidney band 3 anion exchange protein
                                                                                                                                                                                                                                                                                                                                  01-NOV-1991 (Rel. 20, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Band 3 anion transport protein (Anion exchange protein 1) (AE 1).
SLC4A1 OR AE1.
                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND APPEARS TO BE TETRAMERIC.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. IN THE
          Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- TISSUE SPECIFICITY: Kidney.
-i- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                    . 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=2;
     Score 96; DB 1; 1 Pred. No. 2.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                     927 AA.
                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Kidney;
IsoId=P23562-2; Sequence=VSP_000455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=P23562-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGRFAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001717; Anion_exchange.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotransp; 1.
PRINTS; PR01231; HCO3_TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; J04793; AAA40800.1; ALT_INIT.
EMBL; L02943; AAA40801.1; -.
PIR; A33810; A33810.
HSSP; P02730; 1BTS.
                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 264:8185-8192(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Kidney;
MEDLINE=89255254; Pubmed=2722777;
                                                                                                                                                       742 GKASTPGAAQIQEVKEQRI 761
                                                                                                        20
                                                      ;
     100.0%;
ilarity 100.0%;
Conservative 0;
                                                                                                        1 GKASTPGAAAQIQEVKEQRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 46-927 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-45 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=Erythrocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COLLECTING DUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        deduced from a cDNA.
Query Match
Best Local Similarity
Matches 20; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                     B3AT_RAT
P23562;
                                                                                                                                                                                                                                   RESULT 2
                                                                                                                                                                                                                                                             B3AT_RAT
                                                                                                                                                                                                                                                                                                                                       WHEN THE PROOF OF COURT OF THE PROOF OF THE 
                                                                                                        Óλ
                                                                                                                                                       qq
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kopito R.R., Lodish H.F.; Primary structure and transmembrane orientation of the murine anion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Band 3 anion transport protein (Anion exchange protein 1) (AE 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (PROBABLE).
PALMITATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 927;
                                                                                                                                                                                                                                                                                                                                                                                            Missing (in isoform Kidney). /FIId-VSP_000455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-87250387; PubMed-3036795;
Kopito, R.R., Andersson M., Lodish H.F.;
"Structure and organization of the murine band 3 gene.";
J. Biol. Chem. 262:8035-8040(1987).
                                                                                                                                                      EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                                                                    EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUL-1987) to the EMBL/GenBank/DDBJ databases.
                CYTOPLASMIC (POTENTIAL).
MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                 681A228474E5E9DE CRC64;
                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-86034211; PubMed=3840489;
Koptto R.R., Loddish H.F.;
"Structure of the murine anion exchange protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 89; DB 1; 1 Pred. No. 3.4e-06;
  splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              929 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                POTENTIAL. POTENTIAL.
                                                                            POTENTIAL.
                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                   POTENTIAL
Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 11-929 FROM N.A. MEDLINE=86274622; Pubmed=3015590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=85268011; Pubmed=2410791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GKASTPGAAQIQEVKEQRI .20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell. Biochem. 29:1-17(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                     927 AA; 103172 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.7%;
95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exchange protein.";
Nature 316:234-238(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MEB3).
SLC4A1 OR AE1
  Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B3AT_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kopito R.R.
                                                                                                                                                          DOMAIN
TRANSMEM
                                     DOMAIN
TRANSMEM
                                                                                                                                                                                                                                      DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                  TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                            FRANSMEM
                                                                                                                   TRANSMEM
                                                                                                                                   RANSMEM
                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                            TRANSMEN
                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P04919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B3AT_MOUSE
```

ö

```
FT
FT
SO
                                                                                                                                                                                          δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lb.ch).
                                                                                                                                                                                                        after in situ proteolysis.";
Biochim. Biophys. Acta 980:291-298(1989).
-!- FUNCTION: BAND 3 IS THE MAJOR INTEGRAL GLYCOPROTEIN OF THE
-!- FUNCTIONE BAND 3 IS THE MAJOR INTEGRAL GLYCOPROTEIN OF THE
ERYTHROCYTE MEMBRANE. BAND 3 HAS TWO FUNCTIONAL DOMAINS. ITS
INTEGRAL DOMAIN MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS
THE MEMBRANE, WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING
SITES FOR CYTOSKELETAL PROTEINS, GLYCOLYTIC ENZYMES, AND
                                                                                                                                                                                                                                                                                                                                      HEMOGLOBIN.
SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY
SUBURIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY
SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                        Major proteolytic fragments of the murine band 3 protein as obtained
                                                                                                                                                    Raida M., Wendel J., Kojro E., Fahrenholz F., Fasold H., Legrum B.,
Demuth D.R., Showe L.C., Ballantine M., Palumbo A., Fraser P.J., Cloe L., Rovera G., Curtis P.J.;
"Cloning and structural characterization of a human non-erythroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE: PS00220; ANION_EXCHANGER_1; 1.
PROSITE: PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprofein; Anion exchange; Erythrocyte; Lipoprotein; Palmitate; Alternative splicing.
DOMAIN 423 929 MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXOPLASMIC LOOP (POTENTIAL). POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: ERYTHROCYTE.
SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                               Event-Alternative splicing; Named isoforms=2;
                                                                                                             SEQUENCE OF 33-47; 360-375; 382-395 AND 578-590 MEDLINE-89229233; PubMed=2713407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=P04919-2; Sequence=VSP_000454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=Erythrocyte;
IsoId=P04919-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:109393; Slc4a1.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotranspt.
PRINTS; PR01231; HCO3TRNSPORT.
TIGRRAMs; TIGR00834; ae; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X02677; CAA26506.1; -. EMBL; M29379; AAA37187.1; -. EMBL; J02756; AAA37278.1; -. EMBL; X03917; CAA27555.1; -. PIR; A25314; A25314;
                                                         band 3-like protein.";
EMBO J. 5:1205-1214(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P02730; 1BTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name-Kidney;
                                                                                                                                                                         Passow H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP;
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-89039870; PubMed=318555;
MEDLINE-89039870; PubMed=318555;
MEDLINE-89039870; PubMed=318555;
Win H. R.C., Yew N.S., Ansorge W., Voss H., Schwager C.,
Vennstroem B., Zenke M., Engel J.D.;
"Two different mRNAs are transcribed from a single genomic locus
encoding the chicken erythrocyte anion transport proteins (band 3).";
Mol. Cell. Biol. 8:4416-4424(1988).
INTEGRAL DOMAIN BAND 3 IS THE MAJOR INTEGRAL GLYCOPROTEIN OF THE
ERYTHROCYTE MEMBRANE. BAND 3 HAS TWO FUNCTIONAL DOMAINS. ITS
INTEGRAL DOMAIN MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS
THE MEMBRANE, WHEREAS ITS CYTOOLASMIC DOMAIN PROVIDES BINDING
SITES FOR CYTOSKELETAL PROTEINS, GLYCOLYTIC ENZYMES, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBDITT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY AND APPEARS TO BE TETRAMERIC.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-FBB-1996 (Rel. 33, Last annotation update)
Band 3 anion transport protein.
Gallus gallus (Chicken).
Eukaryotä; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRU1201, ....
TIGREMORY TIGREMORY, ae; 1.
PROSITE; PS00220; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Anion exchange; Erythrocyte.
DOMAIN ... 416 MEMBRANE (POTENTIAL).
MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                   Length 929;
                               79 Missing (in isoform Kidney).

/FIGA*VSP_000454.

467 G -> S (IN REF. 5).

103135 MW; 5C0E281C394FB614 CRC64;
     PALMITATE (BY SIMILARITY)

    -!- TISSUE SPECIFICITY: ERYTHRÖCYTE.
    -!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.

                                                                                                                                                                                          Pred. No. 3.4e-06;
                                                                                                                                                                   Score 89; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         922 AA.
                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotransp; 1.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                              1 GKASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                   92.7%;
95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M23404; AAA48753.1; -. HSSP; P02730; 1BTQ.
                                                                                                                                                                                             Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
861
79
                                                                                    467
                                                                                                              929 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HEMOGLOBIN.
     861
1
                                                                                    467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B3AT_CHICK
P15575;
     LIPID
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                              SEQUENCE
                                                                                                                                                                      Query Match
                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
B3AT_CHICK
```

S

us-10-087-464-3.rsp

```
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                 TRANSMEM
                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                            DOMAIN
                                                                           DOMAIN
                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B3A2_MOUSE
   SPECTURE FERTHER FERTHER FERTHER SOLUTION STANTANT SPECTURE SECULIARIES SOLUTION SOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kudrycki K.E., Newman P.R., Shull G.E.,
"CDNA cloning and tissue distribution of mRNAs for two proteins that
are related to the band 3 Cl-/HCO3-exchanger.";
J. Biol. Chem. 265:462-471(1990).
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1991 (Rel. 20, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
SLC4A2 OR AE2 OR B3RP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kopito R.R.; "Functional expression and subcellular localization of an anion
                                                                                                                                                                                        LINKED (GLCNAC. . .) (PROBABLE). FF4ECAD6D6OCFOCF CRC64;
                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lindsey A.E., Schneider K., Simmons D.M., Baron R., Lee B.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exchanger cloned from choroid plexus.";
Proc. Natl. Acad. Sci. U.S.A. 87:5278-5282(1990).
-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
DISTRIBUTION.
                                                                                                                                                                                                                                              Score 61; DB 1; Length 922;
                                   CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXOPLASMIC LOOP (POTENTIAL).
POTENTIAL.
 EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                                                                                                                   5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                        N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                   Pred. No. 0.087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1234 AA.
                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                 POTENTIAL. POTENTIAL.
                                                                                                                 POTENTIAL.
                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HESP, PO2730, 1BTQ.
InterPro, IPR001717; Anion_exchange.
InterPro, IPR003020; HC03_cotranspt.
Pfam, PF00955; HC03_cotransp; 1.
PRINTS; PR01231; HC03TRNSPORT.
IIGRPAMS; TIGR00834; ae; 1.
                                                                                                                                                                                                                                                                                                                                                   ||::|| | | |||||||
753 GKSAVPGERAHIVEVKEQRL 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Stomach;
MEDLINE=90094439; PubMed=2294114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90319095; PubMed=2371270;
                                                                                                                                                                                                                                                                                                                           1 GKASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                              102223 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1991 (Rel. 20, Created)
                                                                                                                                                                                                                                              63.5%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; J05166; AAA40799.1; -
                                                                                                                                                                                                                                                                                     12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A34911.
555
580
615
615
672
774
774
796
855
653
                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A34911;
DOMAIN
TRANSMEM
DOMAIN
                                                                                           TRANSMEM
TRANSMEM
                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                              B3A2_RAT
                                                     FRANSMEM
                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                Query Match
                                                                                                                                 TRANSMEM
                                                                                                                                                                                        CARBOHYD
                                                                           DOMAIN
                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                            B3A2_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SO FIT FIT FIT SO STATES
                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                           οy
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B3A2_MOUSE STANDARD; PRT; 1237 AA.
P13808; Q9ES10; Q9ES11; Q9ES12; Q9ES13;
O1-JAN-1990 (Rel. 13, Created)
O1-JAN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
SLC4A2 OR AE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM A).
MEDLINE=89034212; PubMed=3182834;
Alper S.L., Kopito R.R., Libresco S.M., Lodish H.F.;
"Cloning and characterization of a murine band 3-related cDNA from kidney and from a lymphoid cell line.";
J. Biol. Chem. 263:17092-17099(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY. WEDLINE-SPECIFICATIONOGOJA. Lecanda J., Urtasun R., Medina J.F.; "Molecular cloning and genomic organization of the mouse AE2 anion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
Anion exchange; Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exchanger gene.";
Biochmen. Blochmen. 1276:117-124(2000).
-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
DISTRIBUTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 58; DB 1; Length 1234;
Pred. No. 0.35;
2; Mismatches 5; Indels
                                                                                                                                                                       POTENTIAL.
POTENTIAL.
EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (POTE)
N-LINKED (GLCNAC. . .) (POTE)
N-LINKED (GLCNAC. . .) (POTE)
PALMITATE (BY SIMILARITY).
G -> A (IN REF. 2).
RR -> PG (IN REF. 2).
M -> I (IN REF. 2).
M -> I (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MW; FAB4ED12BB916216 CRC64;
                                                                                     CYTOPLASMIC (POTENTIAL). MEMBRANE (ANION EXCHANGE)
                                                                                                                                                                                                                                        POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=P13808-1; Sequence=Displayed
                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                              PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                      HIS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1066 KAVAPGDKPKIQEVKEQRV 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 KASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ilarity 63.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1166
206
926.
                                                                                                                                                                                                                                                                                                     1003
1050
1129
1192
317
                                                                                                                                                                                                                                                                                                                                                                                                                                      856
866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1156
                                                                                                                                                                                             844
893
911
926
947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=A;
```

ó

9

```
SLC4A2 OR AEZ.
                                                                                                                                                                     B3A2_RABIT
                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                        ileum.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                           Anion
                                                                                                                                                          B3A2_RABIT
                                                                                                                                                 RESULT
 SFF
                                                                                                                 g
                                                                                                                                                                               δλ
                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                TISSUE SPECIFICITY: Isoform a is widely expressed at similar levels in all tissues examined. Isoforms bl and b2 are predominantly expressed in stomach although they are also detected at lower levels in other tissues. Isoform c1 is stomach-specific. Isoform c2 is expressed at slightly higher levels in lung and stomach than in other tissues.
                                                                                                                                                                                                                                                                                                                    A HSSP, P01230; IBTU.

R MGD; MG1:109351; S1c4a2.

R MGD; MG1:109351; S1c4a2.

R InterPro; IPR001717; Anion_exchange.

DR InterPro; IPR003020; HC03_cotranspt.

DR PRIME; PF00955; HC03_cotranspt.

DR PRIME; PR001231; HC03TRNSPRT.

DR PROSITE; PS00220; ANION_EXCHANGER_1; 1.

DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.

DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.

DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.

RW Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;

MICHANGE ANION EXCHANGER.

OCYTOPLASMIC (POTENTIAL).

MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PALMITATE (BY SIMILARITY).
MSSAPRRPASGADSLHT -> MDFLLRPQ (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Missing (in isoform C1).
/FTId=VSP_000460.
ERTSPSPPTQTPHQEAAPRASKGAQTG -> MPAFQEWKSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MSSAPRRPASGADSLHT -> MTQ (in isoform B1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXOPLASMIC LOOP (POTENTIAL).
                                                                        IsoId=P13808-5; Sequence=VSP_000459, VSP_000461;
                                                                                                                                               SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (in isoform C2)
P_000459.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /FTId=VSP_000457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VSP_000458
          IsoId=P13808-2; Sequence=VSP_000458;
                              IsoId=P13808-3; Sequence=VSP_000457;
                                                   IsoId=P13808-4; Sequence=VSP_000460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FTIG=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRO-RICH.
HIS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-SER.
                                                                                                                                                                                                                                                                EMBL, AF255774; AGG23154.1; ...
EMBL, AF255774; AGG23155.1; ...
EMBL, AF255774; AGG23156.1; ...
EMBL, AF255774; AGG23158.1; ...
PIR: A31789; A31789.
HSSP; P02730; 1BTQ.
                                                                                                                                                                                                                                                        EMBL; J04036; AAA65505.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   929
950
1006
1053
1132
1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /ARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                  ö
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B-1996 (Rel. 33, Last sequence update)
B-2003 (Rel. 41, Last annotation update)
exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGREAMS; TIGRO0834; ae; 1.
PROSTIE: PSO0219; ANION_EXCHANGER_1; 1.
PROSTIE: PSO0220; ANION_EXCHANGER_2; 1.
Transmembrane: Glycoprotein; Transport; Antiport; Ion transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=New Zealand white;
MEDILINE=93035730; PubMed=1415547;
Chow A., Dobbins J.W. Tronson P.S., Igarashi P.;
"CDNA cloning and localization of a band 3-related protein from
GLREEAVFGAHGCSVCR (in isoform C2).
                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Am. J. Physiol. 263:G345-G352(1992).
-1- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
DISTRIBUTION.
                                                                                                                           Length 1237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                                                                               Indels
                        /FTId=VSP_000461.
A -> G (IN REF. 2).
W; 1A0782C0071782EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Palmitate.
CYTOPLASMIC (POTENTIAL).
MEMBRANE (ANION EXCHANGE)
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL). POTENTIAL.
                                                                                                                           DB 1;
0.35;
                                                                                                                                                         Pred. No. 0.35
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                           Score 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, $45791; AAB23488.1; --
PIR; A56764; A56764.
HSSP; P02730; 1BT0.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotranspt.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                 || || :||||||:
1069 KAVAPGDKPKIQEVKEQRV 1087
                                                                                                                                                                                                                                   2 KASTPGAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lipoprotein;
                                                 205
136813 1
                                                                                                                                                         63.28;
                                                                                                                              60.4%;
                                                                                                                           Query Match 60.4
Best Local Similarity 63.2
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                 205 20
1237 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anion exchange;
```

POTENTIAL

us-10-087-464-3.rsp

```
TRANSMEM
                                                                                                                                                                                                               SEQUENCE
                                                                                                                                   CARBOHYD
                                                                                                                                                        CARBOHYD
                                                                                                                                                                          CARBOHYD
     TRANSMEM
                                                        TRANSMEM
                                                                              TRANSMEM
                                                                                              DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                         B3A2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
     FT
FT
FT
FT
SO
SO
                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCOCC OS NOT THE SET OF SET O
                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-NIH 2; TISSUE-Organ of Corti;
MEDLINE-9023787; PubMed-9804866;
Mhatre A.N., Charachon G., Alper A.L., Lalwani A.K.;
Mhatre A.N., Charachon G., Alper A.L., Lalwani A.K.;
"The guinea pig cochlear AE2 anion exchanger: cDNA cloning and in situ localization within the cochlea.";
Blochim. Blophys. Acta 1414:1-15(1998).
-1- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          28 CL-2001 (Rel. 40, Last sequence update)
Alson exchange protein 2 (Non-erythroid band 3-like protein) (AE2 anion exchanger).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                        N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
PALMITHE (BY SIMILARITY).
W; 2811D11051552BB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGRFAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
                                                      N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                             ö
                                                                                                                                                                      DB 1; Length 1237;
                                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anion exchange; Lipoprotein; Palmitate.

DOMAIN 1 704
CYTOPLASMIC (POTENTIAL).

DOMAIN 705 1238
POTENTIAL.

TRANSMEM 705 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL. CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                      Score 58; DB 1
Pred. No. 0.35;
                                                                                                                                                                                                                                                                                                                                                                                PRT; 1238 AA
                                                                                                                                                                                                               Mismatches
                   PRO-RICH.
HIS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HC03_cotranspt.
Pfam; PF00955; HC03_cotranspt.
PRINTS; PR01231; HC03TRNSPORT.
                                                                                                                                                                                                                                                                    1069 KAVAPGDKPKIQEVKEQRV 1087
                                                                                                                                                                                                        2;
                                                                                                                                                                                                                                                 2 KASTPGAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF121253; AAD19700.1; -. HSSP; P02730; 1BTQ.
                                                                                                                                                                      60.4%;
63.2%;
                                                                                                                                   1237 AA; 136535
                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                      864
878
1169
                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISTRIBUTION.
                                   74
855
864
878
1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          705
734
734
731
823
845
898
916
                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                                                              B3A2_CAVPO
Q9Z0S8;
                                                      CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                               LIPID
SEQUENCE
TRANSMEM
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
TRANSMEM
                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                               B3A2_CAVPO
                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                           RESULT 8
   SCHEFFF
                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REDLINE-2238257; PubMed-12477932;

RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Nillalon D.K., Muzryb D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Holding M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R. "Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B3A2_HUMAN STANDARD; PRT; 1241 AA.
P04920; Q969L3;
13-AGG-1987 (Rel. 05, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (BND3L).
SLC4A2 OR AE2 OR EPB3L1 OR HKB3 OR MPB3L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-86274622; PubMed=3015590; Demuth D.R., Showe L.C., Ballantine M., Palumbo A., Fraser P.J., Cioe L., Rovera G., Curtis P.J.; "Cloning and structural characterization of a human non-erythroid band 3-like protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                       65 N-LINKED (GLCNAC. . .) (POTENTIAL).
79 N-LINKED (GLCNAC. . .) (POTENTIAL).
70 PALMITATE (BY SIMILARITY).
137358 MW; FA1739862ED5ADBF CRC64;
                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM A).
MEDLINE-92223115; PubMed-1562608;
Gehrig H., Mueller W., Appelhans H.;
"Complete nucleotide sequence of band 3 related anion transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 1238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                     Score 58; DB 1
Pred. No. 0.35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochim. Biophys. Acta 1130:326-328(1992).
                                                                                   POTENTIAL. POTENTIAL.
                                                          POTENTIAL.
                                                                                                                                              PRO-RICH.
HIS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1070 KAVAPGDKPKIQEVKEQRV 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM B1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 375-1241 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein AE2 from human kidney
                                                                                                                                                                                                                                                                                                                                                                                                                    63.2%;
                                                                                                                                                                                                                                                                                                                                                                                        60.48;
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 63.29
Matches 12, Conservative
951
1007
1054
1133
1196
316
88
856
855
879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Human)
                                                                                                                                                                                                                                                                                                                                 AA;
931
985
1033
1088
1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
```

œ

```
Name=FL-AE3
                                                                                                                                                                                                                                       SLC4A3 OR AE3.
                                                                                                                                                                                                                                                                                                                                 Schneider K.;
                                                                                                                                                                          B3A3_MOUSE
   CONFLICT
                      CONFLICT
                                         SEQUENCE
                                                             Query Match
                               CONFLICT
                                                                                                                                                       RESULT 10
B3A3_MOUSE
                                                                                  Matches
  FT
FT
FT
SO
                                                                                                      ò
                                                                                                                      g
                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and a sits content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLGHHHGQGAESDPHVTEPLMGGVPE -> CWGITMVRGLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PALMITATE (BY SIMILARITY).
MSSAPRLPAKGADSFCT -> MTQ (in isoform
                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
Anion exchange; Lipoprotein; Palmitate; Alternative splicing.
DOMAIN 708 1241 MEMBRANE (ANION EXCHANGE).
TRANSMEM 708 731 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRO-RICH.

LLIKKED (GLCNAC. . . ) (POTENTIAL).

N-LINKED (GLCNAC. . . ) (POTENTIAL).

N-LINKED (GLCNAC. . . ) (POTENTIAL).
EMBO J. 5:1205-1214(1986).
-1- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VTPTSPSLSWEVFLR (IN REF. 3).
EL -> DV (IN REF. 1 AND 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXOPLASMIC LOOP (POTENTIAL)
                                                                                                    Isold=P04920-2; Sequence=VSP_000456;
SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL). POTENTIAL.
                            SUBCELLUIAR LOCATION: Integral membrane protein ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                          MIM 109280; -.
GO: GO:0005624; C:membrane fraction; TAS.
GO: GO:0005624; C:membrane fraction; TAS.
GO: GO:0008610; F:anion transport; TAS.
InterPro: IPR001117; Anion_exchange.
InterPro: IPR003020; HCO3_cotranspt.
PRAM: PR00355; HCO3_cotranspt.
PRINTS: PR01231; HCO3TRNSPORT.
IIGRFAMS; TIGR00834; ae: 1.
                                                  Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E -> M (IN REF. 1).
H -> R (IN REF. 1).
D -> G (IN REF. 1).
Q -> R (IN REF. 1).
E -> V (IN REF. 1).
E -> R (IN REF. 1).
MISSING (IN REF. 3).
L -> V (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /FTId=VSP_000456
                                                                               IsoId=P04920-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                               EMBL; X62137; CAA44067.1; -.
EMBL; BC009386; AAH09386.1; -.
EMBL; BC009434; AAH0943.1; -.
EMBL; X03918; CAA27556.1; -.
PIR; S21086; S21086.
HSSP; P02730; 1BTQ.
Genew; HGNC:11028; SLC4A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      933
954
1010
1059
1059
1136
1199
320
859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            859
868
882
1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1036
1091
1163
                                                                                                                                                                                                                                                                    HSSr,
Genew; HGNC
109280;
                                                                                          Name=B1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /ARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIPID
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                    Gaps
AAGAAEDDPLRRTGRP -> RQGQLKMIPSADGAA (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-90075236; Pubmed-2686841;
Kopito R.R., Lee B.S., Simmons D.M., Lindsey A.E., Morgans C.W.,
                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDILINE-44171936; PubMed-8126106;
Morgans C.W., Kopito R.R.;
Generation of truncated brain AE3 isoforms by alternate mRNA processing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Regulation of intracellular pH by a neuronal homolog of the erythrocyte anion exchanger."; Cell 59:927-937(1989).
                                                                                                                                                                       DB 1; Length 1241;
                        REF. 1 AND 3).
Q -> R (IN REF. 1 AND 3).
L -> P (IN REF. 1 AND 3).
MW; B116908C5A71DB77 CRC64;
                                                                                                                                                                                                                                    5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 3 (Neuronal band 3-like protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=P16283-3; Sequence=VSP_000466, VSP_000467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=P16283-2; Sequence=VSP_000464, VSP_000465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - TISSUE SPECIFICITY: NEURONAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F. Cell Sci. 106:1275-1282(1993).
-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                      No. 0.35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1227 AA.
                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=P16283-1; Sequence=Displayed;
                                                                                                                                                                          Score 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A33638; A33638.
HSSP; PO2730; LBTQ.
MGD; MGT:109350; Slc4a3.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfam; PP00955; HCO3_cotranspt.
PRINTS; PR01231; HCO3_TRNSPORT.
                                                                                                                                                                                                         Pred.
                                                                                                                                                                                                                                                                                                                                                 1073 KAVAPGDKPKIQEVKEQRV 1091
                                                                                                                                                                                                                                                                                            2 KASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M28383; AAA37184.1; -. EMBL; S69314; AAB30140.1; -.
                                                       824 824
902 902
1241 AA; 136966
                                                                                                                                                                          60.48;
                                                                                                                                                                                                         63.28;
                                                                                                                                                                                                  Best Local Similarity 63.2
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=311-AE3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=14-AE3;
```

o,

us-10-087-464-3.rsp

```
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 3 (Neuronal band 3-like protein) (Cardiac/brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular cloning, expression, and chromosomal localization of two isoforms of the AE3 anion exchanger from human heart."; Circ. Res. 75:603-614(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM CAE3).
TISSUE-Heart;
Kudo S., Mattei M.-G., Bloor C.M., Fukuda M., Ranney H.M., Xu A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                     InterPro; IPR011717, Anion_exchange.
InterPro; IPR012020; HCO3_cotranspt.
InterPro; IPR003020; HCO3_cotranspt.
Prom; Pr001231; HCO3_cotransp; 1.
PRINTS; PR01231; HCO3_TRNSPORT.
IGREAMS; TIGR00834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Transport; Ion transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yannoukakos D., Stuart-Tilley A., Fernandez H., Fey P., Duyk G.,
                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3EB1620EE011730E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (PO
PALMITATE (BY SIMILARITY).
                                                                                                                                                                                                                           MEMBRANE (ANION EXCHANGE)
                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 54; DB 1;
Pred. No. 1.5;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1232 AA
                                                                                                                                                                                                             CYTOPLASMIC
                                                                                                                                                                                                                                       POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
    send an email to license@isb-sib.ch)
                                                                                                                                                                                             Lipoprotein; Palmitate
                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-LYS.
POLY-SER.
POLY-LEU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-GLU.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                       HIS-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM BAE3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Heart;
MEDLINE-95008042; PubMed-7923606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anion exchange protein 3 (Neuron
band 3-like protein) (CAE3/BAE3)
SLC4A3 OR AE3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last seq
                              EMBL; J05167; AAA40798.1; -. PIR; B34911; B34911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA; 135406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.2%;
61.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 ASTPGAAAQIQEVKEQRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                             044
                                                                                                                                                                                                                                                                                                                                                                                                                      1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
es 11; Conserv
                                                             P02730; 1BTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                               Anion exchange;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alper S.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B3A3_HUMAN
P48751;
                                                                                                                                                                                                                                         TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                        PRANSMEM
                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                             HSSb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B3A3_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                       LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                         /FTIG=VSP_000464.
Missing (in isoform 311-AE3).
/FTIG=VSP_000465.
KPLHMPGGDGHRGKSLK -> FCVLRSPSPCLGETVTEGKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-90094439; PubMed-2294114;
MEDLINE-90094439; PubMed-2294114;
Rudryckí K.E., Newman P.R., Shull G.E.;
Rudryckí K.E., Newman P.R., Shull G.E.;
"EDNA cloning and tissue distribution of mRNAs for two proteins that are related to the band 3 C1-/HC03-exchanger.";
J. Biol. Chem. 265:462-471(1990).
--- FUNCTION: PLASAMA MEMBRARE ANION EXCHANGE PROTEIN.
---- SUBCELLULAR LOCATION: Integral membrane protein.
---- TISSUE SPECIFICITY: NEURONAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                             AALLDLEGTTL -> RAFWAGNESLL (in isoform 311-AE3).
TIGRPAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Transport; Ion transport;
                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                             Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 54; DB 1; Length 1227;
Pred. No. 1.5;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     Missing (in isoform 14-AE3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                /FTId=VSP_000467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1991 (Rel. 20, Last Sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 3 (Neuronal band 3-like protein).
SLC4A3 OR AB3 OR B3RP3.
                                                                          CYTOPLASMIC.
MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (
PALMITATE (BY SIMILARITY
                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                        isoform 14-AE3).
                                                                                                                                                                                                                                                                                                                                                                                                                    'FTId=VSP_000466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1227 AA
                                                             Anion exchange; Lipoprotein; Palmitate;
                                                                                                                      POTENTIAL.
                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                   POTENTIAL.
                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1227 AA; 135164 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1991 (Rel. 20, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.2%;
61.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 ASTPGAAAQIQEVKEQRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 61.1.,
Thos 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                           1227
                                                                                                                                                                                                                                                                                                                                                                                                                                     1227
                                                                                                                                                                                                                                                       1186
                                                                                                                                                                                                                                                                                                                                                                                        503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                    504
                                                                                                                                                                                                                                                                                                                                                             392
                                                                                                                                                                                                                                                                                                                                                                                        487
                                                                                                                                                                                DOMAIN
TRANSMEM
                                                                                                                                                                                                           TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B3A3_RAT
                                                                                                       FRANSMEM
                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                       RANSMEM
                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                                                                           VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                        VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                     VARSPLIC
                                                                                                                        FRANSMEM
                                                                                                                                                  PRANSMEM
                                                                                                                                    RANSMEN
                                                                                                                                                                                                                                         RANSMEN
                                                                          DOMAIN
                                                                                           DOMAIN
                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                   LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B3A3_RAT
    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

ö

Gaps

```
CONFLICT
                                                                                                                                                                                                                B3A3_RABIT
                                                                                                                                                                                                      RESULT 13
   SHARAHAA
                                                                                                                                                                        g
                                                                                                                                                                                                                          ŏ
                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs-sib.ch).
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
DISTRIBUTION. MEDIATES AT LEAST A PART OF THE CL(-)/HCO3(-)
EXCHANGE IN CARDIAC MYOCYTES. BOTH BAE3 AND CAE3 FORMS TRANSPORT
                                                                                                                     ISOId=P48751-2; Sequence=VSP_000462, VSP_000463;
TISSUE.SPECIFICITY: BOTH BAE3 AND CAE3 ARE EXPRESSED IN FAILING
                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein; Transport; Antiport; Ion transport; Inpoprotein; Palmitate; Alternative splicing. CYTOPLASMIC.
9 1232 MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                       MIM; 106195; -
O(0) GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0005684; C:membrane fraction; TAS.
GO; GO:0005624; C:membrane fraction; TAS.
GO; GO:0006832; F:inorganic anion exchanger activity; TAS.
GO; GO:0006832; F:small molecule transport; TAS.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR0030302; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotranspt.
PRINTS; PRO1231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (in isoform CAE3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isoform CAE3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PALMITATE (BY SIMILARITY).
                                                                                                                                                   SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
                                      CL(-).
SUBCELLULAR LOCATION: Integral membrane protein.
                                                                    Event-Alternative splicing; Named isoforms=2;
                                                                              Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Missing (in isofo/
FTId=VSP_000462.
                                                                                                 IsoId=P48751-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> MPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                           TIGREAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-SER.
POLY-LYS.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /FTId=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY - LEU
                                                                                                                                                                                                                                                   EMBL, U05596; AAA50748.1; -.
EMBL, L27213; AAB05850.1; -.
PIR, 138496, 138496.
HSSP, P02730; 1BTQ.
Genew; HGNC:11029; SLC4A3.
MIM; 106195; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Lipoprotein; 708 1232 1731
                                                           ALTERNATIVE PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304
343
466
608
702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1002
1049
1128
1149
149
161
207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187
165
296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299
                                                                                                                                                                                                                                                                                                                                                                                                                                      Anion exchange;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304
343
466
608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297
                                                                                        Name=BAE3;
                                                                                                                                                                                                                                                                                                                                                                                                                           ransmembrane;
                                                                                                            Name=CAE3;
                                                                                                                                           VENTRICLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /ARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIPID
```

ع . .

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation-the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
38-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 3 (Neuronal band 3-like protein) (Anion exchanger 3 brain isoform).
SLC4A3 OR AE3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó;
                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 1232;
                                                                                                                                                                                                                                                                           > M (IN REF. 2).
1825BE15977C3821 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Abuladze N., Pushkin A., Kurtz I.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases
-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEMBRANE (ANION EXCHANGE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: NEURONAL.
-!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
POTENTIAL.
   (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1.5;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1233 AA.
GS -> FI (IN R A -> L (IN R B A -> L (IN R B A -> C (IN R I 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                  Score 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P02730; 1BTQ.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00955; HCO3_cotransp; 1.
PRINTS; PR01231; HCO3TRNSPORT.
TIGRFAMS; TIGR00834; ae; 1.
                                                                                                                                                                                                                                                                                                                  MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1066 AIAPGDKPQIQEVREQRV 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 ASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF031650; AAB86859.1; -.
                                                                                                                                                                                                                                                                                                              135706
                                                                                                                                                                                                                                                                                                                                                                              56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                              61.1%;
                                                                                                                                                                                                                                                                                                                                                                              Query Match 56.2
Best Local Similarity 61.1
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
   813
822
861
867
875
885
887
8887
                                                                                                                                                                                                                                                                           1096
                                                                                                                                                                                                                                                                                                                  ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
   812
822
861
863
875
885
887
887
1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B3A3_RABIT
018917;
                            CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RANSMEM
                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RANSMEN
```

```
Search completed: September 3, 2003, 11:46:57 Job time : 10.25 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- FUNCTION: THIS PROTEIN IS PRÓBABLY A COMPONENT OF THE ACTIVE POLYMERASE. IT MAY FUNCTION IN TEMPLATE BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=88299965; PubMed=3404121;
Takeuchi K., Hishiyama M., Yamada A., Sugiura A.;
"Molecular cloning and sequence analysis of the mumps virus gene encoding the Protein: mumps virus P gene is monocistronic.";
J. Gen. Virol. 69:2043-2049(1988).
                                 N-LINKED (GLCNAC. . .) (POTENTIAL).
PALMITATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                         ö
                                                                                                                                                 Length 1233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 391;
                                                                                                                                                                                                                                                                                                  01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
RNA polymerase alpha subunit (EC 2.7.7.48) (Nucleocapsid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                               Mumps virus (strain Enders).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
NCBI_TaxID=11167;
                                                                                                                            AE486423E9818583 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF03210; Paramyx_P_V; \overline{1}. Transferase; Nucleocapsid; Transferase; RNA-directed RNA polymerase; Nucleocapsid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         391 AA; 41650 MW; 2802A11A5542B7A5 CRC64;
                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.9%; Score 45; DB 1; 52.6%; Pred. No. 12;
                                                                                                                                                                                                                                                                              391 AA
                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                  POLY-GLU.
POLY-SER.
POLY-LYS.
POLY-SER.
                      POTENTIAL.
                                                                                                                                                   Score 54;
  POTENTIAL
                                                         HIS-RICH
                                                                                                                                                               2
                                                                                                                  POLY - LEU
                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interPro; IPR004897; Paramyx_P_V.
                                                                                                                                                                                                             1067 AIAPGDKPQIQEVREQRV 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                              3 ASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D00351; BAA00259.1; -.
                                                                                                                                                  56.2%;
                                                                                                                            135759
                                                                                                                                                               61.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 52.6
Matches 10; Conservative
                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                              STANDARD;
                                             1166
                                                                                                                  1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JU0067; RRNZED.
                                                                                                                              ¥
                                                                                                                                                          Local Similarity
nes 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                  phosphoprotein).
                                                                               203
309
443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [RNA] (N).
                                                                                                                                                                                                                                                                              RRPP MUMPE
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                  CARBOHYD
                                                                                                                            SEQUENCE
                                                                                                                                                   Query Match
                      RANSMEM
                                                         DOMAIN
                                                                    DOMAIN
                                                                                DOMAIN
                                                                                           DOMAIN
                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                      P16072
                                                                                                                  DOMAIN
                                             LIPID
                                                                                                                                                                                                                                                                RRPP_MUMPE
                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                       RESULT 14
                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                   Q
  2555555555555
                                                                                                                                                                                                ŏ
```

pp

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.9%; Score 45; DB 1; Length 391; 52.6%; Pred. No. 12; ive 3; Mismatches 6; Indels
                                             01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
RNA polymerase alpha subunit (EC 2.7.7.48) (Nucleocapsid
                                                                                                                                                                                                        Mumps virus (strain Miyahara vaccine).
Viruses: ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
NCBI_TaxID=11171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR004897; Paramyx_P_V.
Pfam; PF03210; Paramyx_P_V; 1.
Transferase; RNA-directed RNA polymerase; Nucleocapsid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FD7053C9C7BC522C CRC64;
391 AA.
  PRT;
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=88299965; Pubmed=3404121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ||||||| |:|: |
153 KRGGPGAAQGQTIQEEGI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      391 AA; 41587 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D00352; BAA00260.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; JU0066; RRNZYA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
es 10; Conserv
                                                                                                                                                           phosphoprotein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphorylation |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (RNA)(N)
RRPP_MUMPM
P16595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
```

THIS PAGE BLANK (USPTO)

```
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

September 3, 2003, 11:25:42 ; Search time 9.25 Seconds
(without alignments)
101.679 Million cell updates/sec Run on:

US-10-087-464-4 112 1 DRILLLFKPPKYHPDVPYVK 20 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

127863 Total number of hits satisfying chosen parameters:

127863 seqs, 47026705 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P02730 homo sapien		PO4919 mus musculu	P15575 gallus gall	P23347 rattus norv	P13808 mus musculu	P48746 oryctolagus .		Q9z0s8 cavia porce		P23348 rattus norv	P48751 homo sapien	-	homo	Q96dt0 homo sapien	mus n		-	Q38924 arabidopsis	Q64685 mus musculu	P97764 mus musculu	_	_		-	-	Q9uj83 homo sapien					_	P29712 anabaena sp
SUMMARIES	, ID	B3AT_HUMAN	B3AT_RAT	B3AT_MOUSE	B3AT_CHICK	B3A2_RAT	B3A2_MOUSE	B3A2_RABIT	B3A2_HUMAN	B3A2_CAVPO	B3A3_MOUSE	B3A3_RAT	B3A3_HUMAN	B3A3_RABIT	SOC7_HUMAN	LEGC_HUMAN	SOC7_MOUSE	B3AT_ONCMY	UL16_EBV	PPAF_ARATH	SIA1_MOUSE	WBP1_MOUSE	CYNS_ORYSA	YB46_METTH	VNS3_AHSV1	VNS3_AHSV2	VNS3_AHSV8	HPCL_HUMAN	SIA1_RAT	SIA1_HUMAN	NO75_LUPLU	DNLI_THEVO	DM3B_MOUSE	Y458_ANASP
	DB	-	Н	٦	7	~	٦	_	П	٦	П	٦	٦	~	-	7	П	7	٦	7	7	٦	П	-	П	~	٦	7	7	_	-	7	-	
	Query Match Length	911	927	929	922	1234	1237	1237	1241	1238	1227	1227	1232	1233	440	336	436	918	336	469	403	304	168	234	218	218	218	578	403	406	434	288	859	179
ď	Query Match	100.0	96.4	96.4	73.2	66.1	66.1	66.1	66.1	65.2	60.7	60.7	55.4	55.4	51.8	46.4	44.6	44.6	43.8	43.8	42.9	42.4	42.0	42.0	41.1	41.1	41.1	41.1	40.2	40.2	φ.	40.2	40.2	39.3
	Score	112	108	108	82	74	74	74	74	73	99	89	62	62	28	52	20	20	49	49	48	47.5	47	47	46	46	46	46	45	45	45	45	45	44
	Result No.		7	e	4	S	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	22	56	27	28	29	30	31	32	33

058094 methanococc	Q00024 agaricus bi	P70711 rattus norv	P21734 saccharomyc	Q00341 homo sapien	P81021 gallus gall	Q01197 gossypium h	P06503 trichoplusi	O12705 xestia c-ni	P38552 rattus norv	P50108 saccharomyc	Q9uqq2 homo sapien
TKIN METJA	PPO1_AGABI	UB5D_RAT	UBC1_YEAST	VGLN_HUMAN	VGLN_CHICK	E6_GOSHI	GRAN_GVTN	GRAN_GVXN	LEG4_RAT	MN10_YEAST	LNK_HUMAN
7	Н		٦	7	_	П	П	Н	Т	7	Т
274	268	147	215	1268	1270	238	248	248	324	393	575
39.3	39.3	38.8	38.8	38.8	38.8	38.4	38.4	38.4	38.4	38.4	38.4
44	44	43.5	43.5	43.5	43.5	43	43	43	43	43	43
34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	RESULT	
	B3AT_HUMAN ID B3AT_	HUMAN BISAT_HUMAN STANDARD; PRT; 911 AA. POAJZAA.
		21-JUL-1986 (Rel. 01, Created)
	DT UI	01-APR-1990 (Rel. 14, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update)
	DE Ba	Band 3 anion transport protein (Anion exchange protein 1) (AE 1)
		(CD233 dHL19eH). SLC4Al OR AEl OR EPB3 OR DI.
		,
	OC Eu	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Rutheria: Drimates: Catarrhini: Hominidae: Homo
		200 000
	RN [1]	A MODEL
		SECOENCE FROM N.A. MEDLINE=90083213; PubMed=2594752;
		Lux S.E., John K.M., Kopito R.R., Lodish H.F.;
		loning and characterization of band 3, the human erythrocyte anion-
		Proc. Natl. Acad. Sci. U.S.A. 86:9089-9093(1989).
	RP SE	SEQUENCE FROM N.A.
		TINSUE=B1000; MBDLINB=89134172: DubMed=3223947:
		nner M.J.A., Martin P.G., High S.;
		"The complete amino acid sequence of the human erythrocyte membrane
		anion-transport protein deduced from the cDNA sequence.";
	KL BIO	Jeinem, J. 230:/U3"/IZ(I968).
		SEQUENCE OF 1-199; 220-292 AND 347-370.
_		DLINE=90001294; PubMed=2790053;
		nnoukakos D., Vasseur C., Blouquit Y., Bursaux E., Wajcman H.;
		timery setuceute of the Cycopiasmic domain of fundative state of the cycle
	RL Bi	Biochim. Biophys. Acta 998:43-49(1989).
_		
	RP SE	SEQUENCE OF 1-201. Mediine-83238305: Dubmod-6345535.
		of R.K., Murthy S.N.P., Reddy A.G., Steck T.L., Kohler H.:
	RT "A	mino acid sequence of the N alpha-terminal 201 residues of human
		erythrocyte membrane band 3.";
	אני ט. מא	BIOI. Chem. 236:/961-/990(1963).
		DUENCE OF 1-3.
		MEDLINE=79027186; PubMed=701248;
	RA Dr	Drickamer L.K.;
		"Orientation of the band 3 polypeptide from numan erythrocyte membranes Identification of NHO-terminal secuence and site of
		carbohydrate attachment.";
		Biol. Chem. 253:7242-7248(1978).
	KN [b]) DIENCE OF 559-630
		MEDLINE=83308584; Pubmed=6615451;
		Brock C.J., Tanner M.J.A., Kempf C.,
_	KI.	ne numan erythrocyte anion-transport protein. Partial amino acid

```
Pinna L.A., Donella-Deana A.; "Sequential phosphorylation of protein band 3 by Syk and Lyn tyrosine kinases in intact human erythrocytes: identification of primary and secondary phosphorylation sites."; Blood 96:1550-1557(2000).
                                                                          Hamasaki N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT MEMPHIS GLU-56.
MEDLINE=91329825; PubMed=1678289;
Yannoukakos D., Vasseur C., Driancourt C., Blouquit Y., Delauney J.,
Wajcman H., Bursaux E.;
"Human erythrocyte band 3 polymorphism (band 3 Memphis):
characterization of the structural modification (Lys 56-->Glu) by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT HE 400-ALA--ALA-408 DEL, AND VARIANT MEMPHIS GLU-56.
MEDLINE-92107882; PubMed=1722314;
Jarolim P., Palek J., Amato D., Hassan K., Sapak P., Nurse G.T.,
Rubin H.L., Zhai S., Sahr K.E., Liu S.-C.;
"Deletion in erythrocyte band 3 gene in malaria-resistant Southeast
Asian ovalocytosis.";
 conformation and a possible molecular mechanism for anion
                                                                                                                                                                                                                                                                              the
                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION OF TYR-8; TYR-21; TYR-359 AND TYR-904.
MEDLINE-20400020; PubMed-10942405;
Brunati A.M., Bordin L., Clari G., James P., Quadroni M., Baritono
                                             SEQUENCE OF 834-911.
MEDLINE-88228050; PubMed-3372523;
Kawano Y., Okubo K., Tokunaga F., Miyata T., Iwanaga S., Hamasaki "Localization of the pyridoxal phosphate binding site at the COOH-terminal region of erythrocyte band 3 protein.";
J. Biol. Chem. 263:8232-8238(1988).
                                                                                                                                                             Jennings M.L., Smith J.S.;
"Anion-proton cotransport through the human red blood cell band 3 protein. Role of glutamate 681.";
J. Biol. Chem. 267:13964-13971(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Band 3 Tuscaloosa: Pro-327-->Arg substitution in the cytoplasmic domain of erythrocyte band 3 protein associated with spherocytic hemolytic anemia and partial deficiency of protein 4.2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-92167271; PubMed-1538405; Schofield A.E., Tanner M.J.A., Pinder J.C., Clough B., Bayley P.M. Statser W.B.; Gratzer W.B.; Reardon D.M., Cox T.M., Wilson R.J.M., Gratzer W.B.;
                                                                                                                                                                                                                         PALMITOYLATION OF CYS-843.

MEDLINE=91358422; PubMed=1885574;

MEDLINE=91358422; PubMed=1885574;

Okubo K., Hamasaki N., Hara K., Kageura M.;

Palmitoylation of toysteine 69 from the COOH-terminal of band 3 protein in the human erythrocyte membrane. Acylation occurs in the middle of the consensus sequence of F-I-IICLAVL found in band 3 protein and G2 protein of Rift Valley fever virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-92329950; Pubmed-1378323;
Jarolim P., Palek J., Rubin H.L., Prchal J.T., Korsgren C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 88:11022-11026(1991).
                                                                                                                                        665-688
                                                                                                                                       ROLE OF GLU-681, AND SEQUENCE OF (
MEDLINE=92332495; Pubmed=1352774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-93343855; PubMed-8343110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT HE 400-ALA--ALA-408 DEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol. Biol. 223:949-958(1992)
                       Biochem. J. 213:577-586(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein chemistry methods.";
Blood 78:1117-1120(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT HS ARG-327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT HS LEU-868.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ovalocytosis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cohen C.M.;
"Band 3 Tus
  sednence,
                                                                                                                                                                                                                                                                                                                             101
```

```
"Human erythrocyte protein 4.2 deficiency associated with hemolytic anemia and a homozygous 40 glutamic acid-->lysine substitution in the cytoplasmic domain of band 3 (band 3Montefiore).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                erythroid
to the
Bruce L.J., Ray M.M., Lawrence C., Tanner M.J.; "Band 3 HT, a human red-cell variant associated with acanthocytosis and increased anion transport, carries the mutation Pro-868-->Leu in the membrane domain of band 3."; Biochem. J. 293:317-320(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT BLOOD GROUP DI(A)/MEMPHIS-II.
MEDLINE-94266802; PubMed-8206915;
MEDLINE-94266802; PubMed-8206915;
"Baruce L.J., Anstee D.J., Spring F.A., Tanner M.J.;
"Band 3 Memphis variant II. Altered stilbene disulfonate binding and the Disgo (Dia) blood group antigen are associated with the human exythrocyte band 3 mutation Pro-884->Leu.";
J. Biol. Chem. 269:16155-16158(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bozon M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT HS ASP-771.
MEDILE-961236073; PubMed-8547122;
MEDILE-96136073; PubMed-8547122;
Maillet P., Vallier A., Reinhart W.H., Wyss E.J., Ott P., Texier P.,
Baklouti F., Tanner M.J., Delaunay J., Alloisio N.;
"Band 3 Chur: a variant associated with band 3 deficient hereditary
spherocytosis and substitution in a highly conserved position of
transmembrane segment 11.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96225450; PubMed=8640229;
Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,
Ebornwell M., Herbers J., Kugler W., Oezcan R., Pekrun A.,
Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;
"Ankyzin-1 mutations are a major cause of dominant and recessive hereditary spherocytosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS HS SER-147 AND MET-488.
MEDLINE=97351102; PubMed=9207478;
Alloisio N., Texier P., Vallier A., Ribeiro M.L., Morle L., Bozor
Bursaux E., Maillet P., Goncalves P., Tanner M.J., Tamagnini G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Changes in the blood group Wright antigens are associated with mutation at amino acid 658 in human erythrocyte band 3: a site cinteraction between band 3 and glycophorin A under certain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization of 13 novel band 3 gene defects in hereditary spherocytosis with band 3 deficiency."; Blood 88:4366-4374(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANTS HS GLN-760; TRP-760; CYS-808 AND TRP-870.
MEDLINE=95134893; PubMed=7530501;
Jarolim P., Rubin H.L., Brabec V., Chrobak L., Zolotarev A.S.,
Alper S.L., Brugnara C., Wichterle H., Palek J.;
"Mutations of conserved arginines in the membrane domain of err
band 3 lead to a decrease in membrane-associated band 3 and to
phenotype of hereditary spherocytosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jarolim P., Murray J.L., Rubin H.L., Taylor W.M., Prchal J.T., Ballas S.K., Snyder L.M., Chrobak L., Melrose W.D., Brabec V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bruce L.J., Ring S.M., Anstee D.J., Reid M.E., Wilkinson S.,
                                                                                                                                                                                                                                                                               MEDLINE-9322958; Pubmed-8471774; Rybicki A.C., Qiu J.J.H., Musto S., Rosen N.L., Nagel R.L., Schwartz R.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANTS HS ASP-285; GLU-455; PRO-707; PRO-834 AND MET-837.
MEDLINE=97099297; PubMed~8943874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANTS HS LYS-40; CYS-518 AND MET-663 DEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARÍANT BLOOD GROUP WR(A).
MEDLINE-95111140; PubMed-7812009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transmembrane segment 11.";
Br. J. Haematol. 91:804-810(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13:214-218(1996).
                                                                                                                                                                                                               [16]
VARIANT MONTEFIORE LYS-40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blood 81:2155-2165(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blood 85:541-547(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blood 85:634-640(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tanner M.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Palek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [18]
```

```
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                           FRANSMEM
                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                  VARSPLIC
                                                                                                                                                             TRANSMEM
                                                                                                                                                                                      PRANSMEM
                                                                                                                                                                                                   TRANSMEM
                                             FRANSMEM
                                                            FRANSMEM
                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                               TRANSMEM
                                                                                                DOMAIN
                                                                                                                        DOMAIN
                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                              B3AT_MOUSE
                                                                                                                                                                                                                                       CIPID
                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
ò
                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                              Kudrycki K.E., Shull G.E., Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: BAND 3 HAS TWO FUNCTIONEL DOMAINS: ITS INTEGRAL DOMAIN MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS THE MEMBRANE, WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING SITES FOR CYTOSKELETAL AND OTHER PROTEINS (BY SIMILARITY).
-!- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY
                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND APPEARS TO BE TETRAMERIC.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. IN THE
BASOLATERAL MEMBRANE OF INTERCALATED CELLS OF DISTAL TUBULES AND
COLLECTING DUCTS.
                                                                                                                                                                                                                                                                                                                          MEDLINE-89255254; PubMed-2722777;
Kudrycki K.E., Shull G.E.;
"Primary structure of the rat kidney band 3 anion exchange protein
deduced from a cDNA.":
                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Band 3 anion transport protein (Anion exchange protein 1) (AE 1).
                                   ö
         Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGREAMS; TIGRO0834; ae; 1,
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;
                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- TISSUE SPECIFICITY: Kidney.
-i- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event-Alternative splicing; Named isoforms-2;
         100.0%; Score 112; DB 1; 100.0%; Pred. No. 3.2e-09;
                                                                                                                                                 927 AA.
               100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Kidney;
IsoId=P23562-2; Sequence=VSP_000455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P23562-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cctranspt.
Pfan; PF00955; HCO3_cctranspt.
PRINTS; PR01231; HCO37RNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; J04793; AAA40800.1; ALT_INIT.
EMBL; L02943; AAA40801.1; -.
PIR; A33810; A33810.
                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                           Biol. Chem. 264:8185-8192(1989).
                                                                        807 DRILLEKPPKYHPDVPYVK 826
                                                          1 DRILLEKPPKYHPDVPYVK 20
                                                                                                                                                                      01-NOV-1991 (Rel. 20, Created)
                                                                                                                                                                                                                                                                                                 SEQUENCE OF 46-927 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-45 FROM N.A.
       Query Match 100.0
Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTERNATIVE PRODUCTS:
                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name-Erythrocyte;
                                                                                                                                                                                                                                                                                                                                                                deduced from a cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P02730; 1BTS
                                                                                                                                                                                                                         SLC4A1 OR AE1.
                                                                                                                                                                                                                                                                                                              TISSUE=Kidney;
                                                                                                                                                B3AT_RAT
P23562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>+</u>
                                                                                                                       RESULT 2
                                                                                                                                    B3AT_RAT
                                                                                 a
                                                          δ
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kopito R.R., Lodish H.F.; "Primary structure and transmembrane orientation of the murine anion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Band 3 anion transport protein (Anion exchange protein 1) (AE 1)
                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (PROBABLE). PALMITATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 927;
                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXOPLASMIC LOOP (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Missing (in isoform Kidney). /FTId=VSP_000455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                      EXOPLASMIC LOOP (POTENTIAL) POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-87250387; PubMed-3036795;
Kopito, R.R., Andersson M., Lodish H.F.;
"Structure and organization of the murine band 3 gene.";
J. Biol. Chem. 262:8035-8040(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUL-1987) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              927 AA; 103172 MW; 681A228474E5E9DE CRC64;
                  CYTOPLASMIC (POTENTIAL).
MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-86034211; PubMed-3840489;
Kopito R.R., Lodish H.F.;
"Structure of the murine anion exchange protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 108; DB 1;
Pred. No. 1.3e-08;
splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              929 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                     POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                         POTENTIAL. POTENTIAL.
                                                            POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
  Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  823 DRILLFKPPKYHPDVPFVK 842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=85268011; PubMed=2410791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [5]
SEQUENCE OF 11-929 FROM N.A.
MEDLINE-86274622; PubMed=3015590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DRILLLFKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell. Biochem. 29:1-17(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.4%;
95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exchange protein.";
Nature 316:234-238(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MEB3).
SLC4A1 OR AE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B3AT_MOUSE
P04919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kopito R.R.
                                                                                                                           TRANSMEM
TRANSMEM
```

ö

```
δλ
                                                                                                                                            Q
                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its mes by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                               after in situ proteolysis.";
Biochim. Biophys. Acta 980:291-298(1989).
-!- FUNCTION: BAND 3 IS THE MAJOR INTEGRAL GLYCOPROTEIN OF THE
ERYTHROCYTE MEMBRANE. BAND 3 HAS TWO FUNCTIONAL DOMAINS. ITS
INTEGRAL DOMAIN MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS
THE MEMBRANE, WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING
                                                                                                                                                                                                                              SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY ND APPERARS TO BE TETRAMERIC.
SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS:
                                                                                                                      "Major proteolytic fragments of the murine band 3 protein as obtained
                                                                    SEQUENCE OF 33-47; 360-375; 382-395 AND 578-590.
MEDLINE-89229233; PubMed-2713407;
Raida M., Wendel J., Kojro E., Fahrenholz F., Fasold H., Legrum B.,
Demuth D.R., Showe L.C., Ballantine M., Palumbo A., Fraser P.J., Cloe L., Rovera G., Curtis P.J.; "Cloning and structural characterization of a human non-erythroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (PROBABLE).
                                                                                                                                                                                                      SITES FOR CYTOSKELETAL PROTEINS, GLYCOLYTIC ENZYMES, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGRFAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL. EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL). MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY: ERYTHROCYTE. SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Palmitate; Alternative splicing.
                                                                                                                                                                                                                                                                                                                            IsoId=P04919-2; Sequence=VSP_000454;
                                                                                                                                                                                                                                                                                         Name=Erythrocyte;
IsoId=P04919-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A25314; A25314.
HSSP: PO07300; IBTS.
MOD: MGT:109303; Slc4a1.
InterPro: IPR001717; Anion_exchange.
InterPro: IPR0013020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotranspt.
Prints; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X02677; CAA26506.1; --
EMBL; M29379; AAA37187.1; --
EMBL; J02756; AAA37278.1; --
EMBL; X03917; CAA27555.1; --
                                    band 3-like protein.";
EMBO J. 5:1205-1214(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4443
475
475
529
550
560
606
642
642
                                                                                                                                                                                                                                                                                                                 Name=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lipoprotein;
                                                                                                           Passow H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
```

```
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY AND APPEARS TO BE TETRAMERIC.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- TISSUE SPECIFICITY: BRYTHROCYTE.
-1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACROSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-89039870; PubMed=3185555; MEDLINE-89039870; PubMed=3185555; MEDLINE-89039870; PubMed=3185555; MEDLINE-89039870; PubMed=3185555; MEDLINE-89039870; PubMed=3185555; MEDLINE-89039870; PubMed=3.26nke M., Ansorge W.D. D. D. D. Senke M., Engel J.D. D. Sengel J.D. D. Senke M., Engel J.D. D. Sengel J.D. Se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Band 3 anion transport protein.
Gallus gallus (Chiken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                           Score 108; DB 1; Length 929;
Pred. No. 1.3e-08;
                                            79 Missing (in isoform Kidney).
/FIGA-VSD-000454.
167 G -> S (IN REF. 5).
103135 MW; 5C0E281C394FB614 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane; Glycoprotein; Anion exchange; Erythrocyte.
                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENȚIAL).
MEMBRANE (ANION EXCHANGE).
POTENTIAL.
            PALMITATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         922 AA.
                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00219; ANION_EXCHANGER_1; 1. PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P02730; 1BTQ.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DRILLEKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00955; HCO3_cotransp; 1.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                       96.4%;
95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M23404; AAA48753.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIGRFAMS; TIGRO0834; ae;
                                                                                                                                                                                                                                                                                                                            19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
861
79
                                                                                                                             467
929 AA;
                                                                                                                                                                                                                                                                                   test Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1990 (Rel. 01-APR-1990 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9031;
    861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEMOGLOBIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                417
450
473
504
536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B3AT_CHICK
P15575;
        LIPID'
VARSPLIC
                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
TRANSMEM
                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
B3AT_CHICK
                                                                                                                                                                                                                                                                                                                            Matches
```

```
IsoId=P13808-1; Sequence=Displayed;
                                                                                                                                                                                                                                               1166
206
926
1018
1156
                                                                                                                                                 1003
1050
1129
1192
                                                                                                                                                                                                              856
866
878
                                                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exchanger gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLC4A2 OR AE2.
                                                    DOMAIN
TRANSMEM
                                                                                                                               DOMAIN
TRANSMEM
                                                                                                                                                                      TRANSMEM
TRANSMEM
                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                    PRANSMEM
                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                         TRANSMEM
                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                     RANSMEM
                                                                                                                                                  TRANSMEM
                                                                                                                                                               RANSMEM
                                                                                                                                                                                                      DOMAIN
                                           DOMAIN
                                                                                                        DOMAIN
                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                 B3A2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                            ö
                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    Kudrycki K.E., Newman P.R., Shull G.E.;
"coDN cloning and tissue distribution of mRNAs for two proteins that
are related to the band 3 Cl./HCO3-exchanger.";
J. Biol. Chem. 265:462-471(1990).
                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                             01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
SLC4A2 OR AE2 OR B3RP2.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kopito R.R.;

"Functional expression and subcellular localization of an anion exchanger cloned from choroid plexus.";

Proc. Natl. Acad. Sci. U.S.A. 87:5278-5282(1990).

-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE DISTRIBUTION.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                            ;
0
                                                                                                        N-LINKED (GLCNAC. . .) (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lindsey A.E., Schneider K., Simmons D.M., Baron R., Lee B.S.,
                                                                                                                                      Score 82; DB 1; Length 922, Pred. No. 0.00011;
 EXOPLASMIC LOOP (POTENTIAL).
                              POTENTIAL.
EXOPLASMIC LOOP (POTENTIAL)
POTENTIAL.
                                                                                                                                                            4; Indels
                      CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                          PRT; 1234 AA.
                                                                                                                                                             Mismatches
                                                                         POTENTIAL. POTENTIAL.
                                                                POTENTIAL.
                                                                                               POTENTIAL.
           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001117; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfam: PF00955; HCO3_cotransp; 1.
PRIWTS; PR01231; HCO3TRNSPORT.
IIGRFAMS; TIGR00834; ae; 1.
                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
IISSUE-Stomach;
MEDLINE-90094439; PubMed-2294114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=90319095; PubMed=2371270;
                                                                                                                                                                                             1 DRILLEKPPKYHPDVPYV 19
                                                                                                                                                            ;
0
                                                                                                                    .
Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; J05166; AAA40799.1; -.
                                                                                                                                      73.2%;
illarity 78.9%;
Conservative
                                                                                                                   102223
                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A34911; A34911.
HSSP; P02730; 1BTQ.
                                                                                                                   922 AA;
                                                                                                                                                 Local Similarity
hes 15; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Brain;
DOMAIN
TRANSMEM
DOMAIN
                                                    TRANSMEM
TRANSMEM
                                                                                    TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                         B3A2_RAT
                               TRANSMEM
                                                                                                        CARBOHYD
                                                                                                                   SEQUENCE
                                                                                                                                       Query Match
                                                                         TRANSMEN
                                           DOMAIN
                                                                                                                                                           Matches
                                                                                                                                                                                                                                    RESULT 5
B3A2_RAT
 FTTTTTTTT
                                                                                                                                                                                 ð
                                                                                                                                                                                                    셤
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B3A2_MOUSE STANDARD; PRT; 1237 AA.
P13808; Q9ES09; Q9ES10; Q9ES11; Q9ES12; Q9ES13;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIS ACCH.

N-LINKED (GLCNAC. . . ) (POTENTIAL).

N-LINKED (GLCNAC. . . ) (POTENTIAL).

N-LINKED (GLCNAC. . . ) (POTENTIAL).

PALMITATE (BY SIMILARITY).

G -> A (IN REF. 2).

R -> I (IN REF. 2).

M -> I (IN REF. 2).

M -> I (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM A).
MEDLINE-89034212; PubMed=3182834;
Alper S.L., Kopito R.R., Libresco S.M., Lodish H.F.;
"Cloning and characterization of a murine band 3-related cDNA from kidney and from a lymphoid cell line.";
J. Biol. Chem. 263:17092-17099(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lecanda J., Urtasun R., Medina J.F.; ^{*} "Molecular cloning and genomic organization of the mouse AE2 anion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Sukaiyota; Metaazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
MEDLINE-20462926; PubMed-11006093;
                                                     Antiport; Ion transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. Biophys. Res. Commun. 276:117-124(2000).
-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
- DISTRIBUTION.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 74; DB 1; Length 1234; Pred. No. 0.0025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                              POTENTIAL. EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW; FAB4ED12BB916216 CRC64;
                                                                                                                                  MEMBRANE (ANION EXCHANGE)
                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                           CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                            Palmitate.
                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DRILLLFKPPKYHPDVPYVK
                                                                                  Anion exchange; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.1%;
65.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 66.1
Best Local Similarity 65.0
Matches 13; Conservative
```

.; 0

```
SLC4A2 OR AEZ
                                                                                                                                                                  B3A2_RABIT
                    CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RANSMEN
                                                                                                                                                                            P48746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                              ileum.
                                                                                                                                                        B3A2_RABIT
                                                                                                               qq
                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                              TISSUE SPECIFICITY: Isoform a is widely expressed at similar levels in all tissues examined. Isoforms bl and b2 are predominantly expressed in stomach although they are also detected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTId=VSP_000460.
ERTSPSPPTQTPHQEAAPRASKGAQTG -> MPAFQEWKSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> MDFLLRPQ (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /FTId=VSP_000457.
MSSAPRRPASGADSLHT -> MTQ (in isoform B1).
                                                                                                            at lower levels in other tissues. Isoform c1 is stomach-specific. Isoform c2 is expressed at slightly higher levels in lung and stomach than in other tissues.
                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PR01231; HULLINGER 1.
PROSITE; PS00219; ANION EXCHANGER 1; 1.
PROSITE; PS00220; ANION EXCHANGER 2; 1.
Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
Anion exchange; Lipoprotein; Palmitate; Alternative splicing.

1 703 CYTOPLASMIC (POTENTIAL).

MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL. EXOPLASMIC LOOP (POTENTIAL).
                                                                      Sequence=VSP_000459, VSP_000461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PALMITATE (BY SIMILARITY)
                                                                                                                                             SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Missing (in isoform C1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Missing (in isoform C2) /FTId=VSP_000459.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MSSAPRRPASGADSLHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FTIG=VSP_000458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC
        IsoId=P13808-2; Sequence-VSP_000458;
                              IsoId=P13808-3; Sequence=VSP_000457;
                                                 IsoId=P13808-4; Sequence=VSP_000460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-SER.
                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotransp; 1.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                     EMBL, AF255774; AAG23155.1; EMBL, RES55774; AAG23156.1; EMBL; AF255774; AAG23158.1; EMBL, AF255774; AAG23157.1; PIR, A1789; A31789; A31789; A31789; AGD, MGD, MGD; MGI:109351; S1C4a2.
                                                                                                                                                                                                                                                 EMBL; J04036; AAA65505.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17
                                                                     IsoId=P13808-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167
                    Name=B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /ARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics. Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                          ö
                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00219; ANION EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Iransmembrane; Glycoprotein; Transport; Antiport; Ion transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-NOW Zealand white;
MEDILINE-93035730; Pubmed=1415547;
Chow A., Dobbins J.W. Aronson P.S., Igarashi P.;
"Chow A. Dobbins J.W. Aronson P.S., Igarashi P.;
GLREEAVFGAHGCSVCR (in isoform C2).
                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Am. J. Physiol. 263:G345-G352(1992).
-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE DISTRIBUTION.
                                                                                                                                  Length 1237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                                                                                          4; Indels
                      /FTIG=VSP_000461.
A -> G (IN REF. 2).
W: 1A0782C0071782EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
MEMBRANE (ANION EXCHANGE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL)
                                                                                                                                  DB 1;
0.0025;
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1237 AA
                                                                                                                                                                                     3; Mismatches
                                                                                                                                  Score 74;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, S45791; AAB23488.1; -.
PIR, A56764, A56764.
HSSP, P02730; 1BTQ.
Interpro; IPR001317; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
                                                                                                                                                                                                                                                                     1 DRILLLEKPPKYHPDVPYVK 20
                                                  205 A -. 136813 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00955; HC03_cotransp; 1.
PRINTS; PR01231; HC03TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lipoprotein;
                                                                                                                                Query Match 66.1%;
Best Local Similarity 65.0%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGRFAMs; TIGR00834; ae; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                  205 2C
1237 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anion exchange;
```

```
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIPID
       <u>'</u>.
                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-22388257; PubMed-12477932;

MEDLINE-22388257; PubMed-12477932;

MEDLINE-22388257; PubMed-12477932;

MEDLINE-22388257; PubMed-12477932;

MEDLINE-22388257; PubMed-12477932;

MEDLINE-22388257; PubMed-124.77932;

MEDLINE-22388257; PubMed-124.77932;

MEDLINE-22388257; PubMed-124.77932;

MEDLINE-22388257; PubMed-124.77932;

MEDLINE-22388257; PubMed-124.77932;

MEDLINE-22388257; PubMed-124.77 Max S.I., Wang J., Haiseh F., Bratchento L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Rab Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Rab S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Rownstein M.J., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M., Rahes J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Makesley R.W., Touchman J.W., Green E.D., Dickson M.C., R. Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., M. Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., H. C., L. C., L., Marra M.A., Marra M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B3A2_HUWAN STANDARD; PRT; 1241 AA.
P04920; 0969L3;
13-AGG-1987 (Rel. 05, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (BND3L).
SLC4A2 OR AEZ OR EPB3L1 OR HKB3 OR MPB3L.
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECURINE-86274622; PubMed-3015590;
Demuth D.R., Showe L.C., Ballantine M., Palumbo A., Fraser P.J.,
Cloe L., Rovera G., Curtis P.J.;
"Cloning and structural characterization of a human non-erythroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                   N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
PALMITATE (BY SIMILARITY).
WW. 2811D11051552BB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM A).
MEDLINE-92223115, PubMed-1562608;
Gehrig H., Mueller W., Appelhans H.;
"Complete nucleotide sequence of band 3 related anion transport
                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         band 3-11ke protein.";
EMBO 0. 5:1205-1214(1986).
-i- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
DISTRIBUTION.
                                                                                                                                                                                                                Length 1237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                   Score 74; DB 1;
Pred. No. 0.0025;
                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochim. Biophys. Acta 1130:326-328(1992).
                                               HIS-RICH.
                                                                                                                                                                                                                                                                                                                                          :|: || |||:||| |||
1133 ERLHLLLMPPKHHPDVTYVK 1152
                                               74 88 HIS-F
855 855 N-LIP
864 864 N-LIP
878 878 N-LII
1169 1169 PALMI
1237 AA; 136535 MW;
                                                                                                                                                                                                                                                                                                                 1 DRILLLFKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM B1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein AE2 from human kidney
                                                                                                                                                                                                                66.1%;
65.0%;
                                                                                                                                                                                                                                                                    13; Conservative
                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                     CARBOHYD
CARBOHYD
CARBOHYD
TRANSMEM
DOMAIN
DOMAIN
                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          B3A2_HUMAN
                                                                                                                                             LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHEFFFF
                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                              q
```

SUBCELLULAR LOCATION: Integral membrane protein.

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /FTId=VSP_000456.
E -> M (IN REF. 1).
E -> M (IN REF. 1).
D -> G (IN REF. 1).
C -> V (IN REF. 1).
E -> R (IN REF. 1).
E -> R (IN REF. 1).
L -> V (IN REF. 1).
L -> V (IN REF. 1).
L -> V (IN REF. 1).
LLGHHHGGGAESDPHVTEPLMGGVPE -> CWGITMVRGLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MSSAPRLPAKGADSFCT -> MTQ (in isoform B1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EL -> DV (IN REF. 1 AND 3).
AAGAAEDDPLRRTGRP -> RQGQLKMIPSADGAA (IN
                                                                                                                                                                                                                                                                                                                                                                                                      Prom., Prom. 1.
Print. 1.
Print. 2.
Print. 2.
Print. 2.
Prostre: Ps00219; ANION_EXCHANGER_1; 1.
PROSTRE: Ps00220; ANION_EXCHANGER_2; 1.
Transmembrane: Glycoprotein: Transport; Antiport; Ion transport; Anion exchange; Lipoprotein: Palmitate; Alternative splicing. Anion exchange; Lipoprotein: Cyroplasmic (Potemrial).

1.01
MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
PALMITATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VTPTSPSLSWEVFLR (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL. EXOPLASMIC LOOP (POTENTIAL).
                                                                           ISOId=P04920-2; Sequence=VSP_000456; SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REF. 1 AND 3).
Q -> R (IN REF. 1 AND 3).
L -> P (IN REF. 1 AND 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                       MIM; 109280; -.
GO; GO:0005624; C:membrane fraction; TAS.
GO; GO:0008609; F:anion transporter activity; TAS.
GO; GO:0006820; F:anion transport; TAS.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotranspt.
PRINTS; PR01231; HCO3TRNSPORT.
            Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                   IsoId=P04920-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRO-RICH
                                                                                                                                                                                                                                     EMBL, BC009386; AAH09386.1; --
EMBL, BC009434, AAH09434.1; --
EMBL, X03918; CAA27556.1; --
PIR; S21086; S21086.
HSSP, POZ730, 1BTO.
Genew, HGNC.11028; SLC4A2.
MIM; 109280.
                                                                                                                                                                                                                           EMBL; X62137; CAA44067.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               954
1010
1059
1136
11199
320
859
868
868
882
1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68
74
92
92
1122
1157
124
399
447
447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         486
681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 824
902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1163
                                                               Name=B1;
                                      Name=A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
```

œ

```
Best Local Similarity
                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=311-AE3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=14-AE3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=FL-AE3;
                                                                                                                                                                                                                                                                                                                                          Schneider K.;
                                                                                                                                                                                B3A3_MOUSE
         CARBOHYD
CARBOHYD
                                         SEQUENCE
                                                              Query Match
                                                                                                                                                           RESULT 10
B3A3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP;
                              LIPID
                                                                                  Matches
                                                                                                                                                                                 FT
                                                                                                       δý
                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                        ö
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=NIH 2; TISSUE-Organ of Corti;
STRAIN=NIH 2; TISSUE-Organ of Corti;
STRAIN=99023787; PubMed=9804866;
Mhatre A.N., Charachon G., Alper A.L., Lalwani A.K.;
The guinea pig cochlear AE2 anion exchanger: cDNA cloning and in situ localization within the cochlea.";
Biochim. Biophys. Acta 1414:1-15(1998).
                                        Gaps
                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
LoCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last anotation update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (AE2
                                                                                                                                                                                                                      Cavia porcellus (Guinea pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
Anion exchange; Lipoprotein; Palmitate.
                                        ò
                  Length 1241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXOPLASMIC LOOP (POTENTIAL). POTENTIAL.
                                        4; Indels
136966 MW; B116908C5A71DB77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                  -1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEMBRANE (ANION EXCHANGE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
                 Score 74; DB 1;
Pred. No. 0.0026;
                                                                                                                                      PRT; 1238 AA
                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; PO2730; 1BTQ.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HC03_cotranspt.
Pfam; PF00955; HC03_cotranspt. 1.
PRINTS; PR01231; HC03TRNSPORT.
ITGRAMS; TIGRO0834; ae; 1.
PROSITE; PS00229; ANION_EXCHANGER_1; 1.
PROSITE; PS00229; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
POTENTIAL.
PRO-RICH.
HIS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                        .1 DRILLERPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF121253; AAD19700.1; -.
                   66.1%;
65.0%;
                                        13; Conservative
                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1054
1133
1196
316
88
 1241 AA;
                              Best Local Similarity
                                                                                                                                                                                                   exchanger).
                                                                                                                                                                                                                                                      NCBI_TaxID=10141;
                                                                                                                                                                                                            SLC4A2 OR AE2
                                                                                                                                     B3A2_CAVPO
Q9Z0S8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
TRANSMEM
TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                    anion
                                        Matches
                                                                                                                 RESULT
S
                                                                                                                                     ö
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
   N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kopito R.R., Lee B.S., Simmons D.M., Lindsey A.E., Morgans C.W.,
                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Morgans C.W., Kopito R.R.; "Generation of truncated brain AE3 isoforms by alternate mRNA processing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Regulation of intracellular pH by a neuronal homolog of the erythrocyte anion exchanger."; Cell 59:927-937(1989).
                                                                                                                                                                                           Score 73; DB 1; Length 1238;
Pred. No. 0.0036;
                                                                                           PALMITATE (BY SIMILARITY).
W; FA1739862ED5ADBF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FB2-2003 (Rel. 41, Last annotation update)
Anion exchange protein 3 (Neuronal band 3-like protein).
SLC4A3 OR AE3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=P16283-3; Sequence-VSP_000466, VSP_000467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=P16283-2; Sequence=VSP_000464, VSP_000465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- TISSUE SPECIFICITY: NEURONAL.
-!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. cell Sci. 106:1275-1282(1993)
--- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN.
--- SUBGEELLILAR LOCATION: Integral membrane protein
--- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING. MEDLINE-94171936; PubMed-8126106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1227 AA.
                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=P16283-1; Sequence=Displayed;
                                                                                                                                                                                           Score 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:109350; Sic4a3.
InterPro; IPR001717; Anion exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfam: PF00955; HCO3_cotranspt.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                           :|: || |||:||| ||||
1134 ERLHLLLMPPKHHPDVMYVK 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE-90075236; PubMed-2686841;
                                                                                                                                                                                                                                                                                                                       1 DRILLFKPPKYHPDVPYVK 20
856 856
865 865
879 879
1170 1170
1238 AA; 137358 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M28383; AAA37184.1; -. EMBL; S69314; AAB30140.1; -.
                                                                                                                                                                                           65.2%;
                                                                                                                                                                                                                           65.0%;
                                                                                                                                                                                                                                                         13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A33638; A33638.
```

```
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 3 (Neuronal band 3-like protein) (Cardiac/brain
band 3-like protein) (CAE3/BAE3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular cloning, expression, and chromosomal localization of two isoforms of the AE3 anion exchanger from human heart."; Circ. Res. 75:603-614(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Heart;
Kudo S., Mattei M.-G., Bloor C.M., Fukuda M., Ranney H.M., Xu A.;
                                                            HSSP; P02730; IBTQ.
InterPo; IPR001717; Anion_exchange.
InterPo; IPR00320; HC03_cotranspt.
Pfam; PF00955; HC03_cotranspt.
PRINTS; PR01231; HC03_cotransp; 1.
PRINTS; PR01231; HC03_COTRNSPORT.
IIGREAMS; TIGR00834; ae; 1.
PROSITE; PS00220; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Transport; Anion exchange; Lipoprotein; Palmitate.
Anion exchange; Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Heart;
MEDLINE-55008042; PubMed-7923606;
Yannoukakos D., Stuart-Tilley A., Fernandez H., Fey P., Duyk G.,
                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL).
PALMITATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 68; DB 1; Length 1227; Pred. No. 0.021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3EB1620EE011730E CRC64;
                                                                                                                                                                                                                                 MEMBRANE (ANION EXCHANGE)
                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1232 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                   CYTOPLASMIC
                                                                                                                                                                                                                                                            POTENTIAL. POTENTIAL.
       or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-GLU.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-LYS.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM BAE3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM CAE3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:||:| | |:||: |||
1125 RLLLIFMPAKHHPEQPYV 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19
                                   EMBL; J05167; AAA40798.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.78;
61.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA; 135406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 RILLLFKPPKYHPDVPYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 60.7
Best Local Similarity 61.1
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                               868
1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1182
                                                                                                                                                                                                                                                                                                                                                                    044
                                                                                                                                                                                                                                                                                                                                                                                                1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                 PIR; B34911; B34911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B3A3_HUMAN
P48751;
                                                                                                                                                                                                                                 DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                     TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                            TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                       RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                  PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                   RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                 PRANSMEM
                                                                                                                                                                                                                                                                                           RANSMEM
                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B3A3_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
       硆
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                /FTIG-VSP_000464.
Missing (in isoform 311-AE3).
/FTIG-VSP_000465.
/FTIG-SPECTORESPECTGETVTEGKA (in isoform 14 AE3).
/FTIG-VSP_000466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AALLDLEGITL -> RAFWAGNESLL (in isoform 311-AE3).
TIČRFAMS; TICRO0834; ae; 1.
PROSITE; PSO0219; ANION_EXCHANGER_1; 1.
PROSITE; PSO0220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Transport; Antiport; Ion transport; Anion exchange; Lipoprotein; Palmitate; Alternative splicing.
                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. . .) (POTENTIAL)
PALMITATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 1227; 0.021;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Missing (in isoform 14-AE3).
/FTId=VSP_000467.
W: D5BEC46E03F4251C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 20, Last sequence update)
Anion exchange protein 3 (Neuronal band 3-like protein).
SLC4A3 OR AE3 OR B3RP3.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- TISSUE SPECIFICITY: NEURONAL.
                                                                                           MEMBRANE (ANION EXCHANGE)
                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1227 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                               CYTOPLASMIC
                                                                                                                         POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                              POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 68;
Pred. No.
                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                    POTENTIAL
                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1125 RLLLIEMPAKHHPEQPYV 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1227 AA; 135164 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 RILLLFKPPKYHPDVPYV 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.7%;
61.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 61.1.
The conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                  1227
                                                                                                                                                                                                                                                                                                                                                                                                                                           1227
                                                                                                                                                                                                                                                                                                                                                                                                503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                           504
                                                               Anion exchange;
DOMAIN 1
                                                                                                                                                                                                                                                                                                                                                                  392
                                                                                                                                                                                                                                                                                                                                                                                                487
                                                                                          DOMAIN
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B3A3_RAT
                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                     ARSPLIC
                                                                                                                                                                                                                                                                                                                                                                  VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                           VARSPLIC
                                                                                                                                                                    FRANSMEM
                                                                                                                                                                                                  FRANSMEM
                                                                                                                                                                                                                PRANSMEM
                                                                                                                                                                                                                                                             RANSMEM
                                                                                                                                        FRANSMEN
                                                                                                                                                        FRANSMEN
                                                                                                                                                                                                                                PRANSMEN
                                                                                                                                                                                                                                              RANSMEN
                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B3A3_RAT
```

ö g ö

Gaps

```
CONFLICT
                                                                                                                                                                                                              B3A3_RABIT
  FIFFFFF
                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PLASMA MEMBRANE ANTON EXCHANGE PROTEIN OF WIDE
DISTRIBUTION. MEDIATES AT LEAST A PART OF THE CL(-)/HCO3(-)
EXCHANGE IN CARDIAC MYOCYTES. BOTH BAR3 AND CAE3 FORMS TRANSPORT
                                                                                                                     'Isold=P48751-2; Sequence=VSP_000462, VSP_000463;
TISSUE SPECIFICITY: BOTH BAE3 AND CAE3 ARE EXPRESSED IN FAILING
                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane, Glycoprotein, Transport, Antiport, Ion transport, Anion exchange, Lipoprotein, Palmitate, Alternative splicing. OWAIN 1 708
                                                                                                                                                                                                                                                                                                            GO: GO:0005887; C:integral to plasma membrane; TAS.
GO: GO:0005624; C:membrane fraction; TAS.
GO: GO:0005624; C:membrane fraction; TAS.
GO: GO:0006812; P:inorganic anion exchanger activity; TAS.
GO: GO:0006812; P:small molecule transport; TAS.
InterPro: IPR003177; Anion_exchange.
InterPro: IPR003177; Anion_exchange.
InterPro: IPR00317; Anion_exchange.
PRINTS; PR0055; HCO3_cotranspt.
PRINTS; PR01231; HCO3_cotranspt.
IGRPAMS; TIGR00834; ae; 1.
PROSITE; PS00220; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPS -> MPA (in isoform CAE3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Missing (in isoform CAE3). /FTId=VSP_000462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PALMITATE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEMBRANE (ANION EXCHANGE)
                                                                                                                                                    SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL). POTENTIAL).
                                                 SUBCELLULAR LOCATION: Integral membrane protein ALTERNATIVE PRODUCTS:
                                                                   Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
Name=BAE3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /FTId-VSP_000463.
                                                                                                 IsoId=P48751-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
POLY-GLU.
PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-LYS.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-LEU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Missing
                                                                                                                                                                                                                                                    Anion exchange; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1187
1165
296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          910
925
946
1002
1049
1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304
343
466
608
702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297
                                                                                                              Name=CAE3
                                                                                                                                                                                                                                                                                                       106195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 3 (Neuronal band 3-like protein) (Anion exchanger 3 brain isoform).
SLC4A3 OR AE3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 1232;
                                                                                                                                                                                                                                                                                                               1825BE15977C3821 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Kidney;
Abuladze N., Pushkin A., Kurtz I.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEMBRANE (ANION EXCHANGE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- SUBCELLUIAR LOCATION: Integral membrane protein.
-i- TISSUE SPECIFICITY: NEURONAL.
-i- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
GS -> FI (IN REF. 2).
F -> L (IN REF. 2).
A -> S (IN REF. 2).
EGSLA -> D (IN REF. 2).
S -> G (IN REF. 2).
S -> G (IN REF. 2).
S -> G (IN REF. 2).
L -> P (IN REF. 2).
L -> P (IN REF. 2).
I -> M (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                             0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                          Score 62;
                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP, P02730; IBTQ.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00955; HCO3_cotransp; 1. PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anion exchange; Lipoprotein; population exchange; Lipoprotein; population exchange; Lipoprotein; population exchange; Lipoprotein; population and the second population and th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 RILLLFKPPKYHPDVPYV 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF031650; AAB86859.1; -.
                                                                                                                                                                                                                                                                                                                                                                              55.4%;
                                                                                                                                                                                                                                                                                                               135706
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
      813
822
861
867
875
885
887
899
                                                                     861
863
875
875
885
887
887
899
1096
1232 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Simi
Matches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B3A3_RABIT
018917;
                                                                                                                                                                                                                                                                            CONFLICT
                                         CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
```

253 DEILQLETPPKYHTQIDYV 271

g

```
HGNC:15788; LGALS12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew; HGNC:157
MIM; 606096; -.
                                                                                                                                                                                                                                                                                                                                                                                         Name=B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=F;
                                                                                                                                                                                                                                                                                                                                                                                                             Name=C;
                                                                                                                                                                                                                                                                                                                                                                         Name-A;
                                                                                                                                                                                                                                                                                                                                                                                                                               Name=D;
                                      LEGC_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                             RESULT 15
                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                         Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
- PUNCTION: SOCS family proteins form part of a classical negative feedback system that regulates cytokine signal transduction.
- SIMILARITY: Contains 1 SH2 domain.
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                            IAC. . .) (POTENTIAL).
SIMILARITY).
                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SH2 domain; Growth regulation; Signal transduction inhibitor. DOMAIN 286 381 SH2.
                                                                                                                          Score 62; DB 1; Length 1233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.8%; Score 58; DB 1; Length 440; 57.9%; Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Indels
                                                                                                                                             4; Indels
                                                                                                        AE486423E9818583 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A4A747AB7F6FF08C CRC64;
                 POTENTIAL.
N-LINKED (GLCNAC.
PALMITATE (BY SIN
                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Suppressor of cytokine signaling 7 (SOCS-7).
SOCS7 OR SOCS4.
                                                                                                                                  Pred. No. 0.17;
4; Mismatches
                                                                                                                                                                                                                                  440 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                              HIS-RICH.
POLY-GLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOCS BOX.
                                                                 POLY-SER
                                                                                     POLY-SER
                                                                                               POLY-LEU
                                                                                                                                                                          1 DRILLLEKPPKYHPDVPYV 19
                                                                                                                                                               2 RILLLFKPPKYHPDVPYV 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50623 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF424815; AAL60517.1; -.
                                                                                                                         / Match 55.4%;
Local Similarity 55.6%;
nes 10; Conservative
                                                                                                        135759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probom: PD000093; SH2; 1. SMART; SM00252; SH2; 1. SMART; SM000253; SCGS; 1. PROSITE; PS50001; SH2; 1. PROSITE; PS50025; SCCS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:19392; SOCS7.
InterPro; IPR000980; SH2.
InterPro; IPR001496; SOCS.
Pfam; PF00017; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 57.9
Matches 11; Conservative
                                                                                                                                                                                                                                  STANDARD;
                                                                                                        1233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     440 AA;
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                         136
203
309
443
                                                                                                                                                                                                                                  SOC7_HUMAN
TRANSMEM
TRANSMEM
TRANSMEM
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                        SEQUENCE
                                                                                                                           Query Match
                                              DOMAIN
                                                                DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                           O8WXH5
                                                                                                                                                                                                              RESULT 14
SOC7_HUMAN
                                      LIPID
                                                                                                                                            Matches
                                                                                                                                                                                  a
                                                                                                                                                                                                                                           ò
 ò
```

= = = =

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isold=096DT0-6; Sequence=VSP_003099, VSP_003101;
-!- TISSUE SPECIFICITY: Not widely expressed. Predominantly expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in adipose tissue.
-i- DOMAIN: CONTAINS TWO HOMOLOGOUS BUT DISTINCT CARBOHYDRATE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hotta K., Firedon, Matsukawa Y., Takahashi M., Nishizawa H., Kishida K., Matsuda M., Kuriyama H., Kihara S., Nakamura T., Tochino Y., Bodkin N.L., Hansen B.C., Matsuzawa Y.; "Galectin-12, an adlpose-expressed galectin-like molecule possessing apoptosis-inducing activity.";
J. Biol. Chem. 276:34089-34097(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Retina;
MEDI.NE-21283005; PubMed=11283015;
Yang R.-Y., Hsu D.K., Yu L., Ni J., Liu F.-T.;
"Cell cycle regulation by galectin-12, a new member of the galectin superfamily.";
                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
LEGC_HUMAN STANDARD, PRT; 336 AA.
096DTG; Q96DS9; Q96PR9; Q9H258; Q9H259; Q9N202;
28 FFBB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Galectin-12 (Galectin-related inhibitor of proliferation).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -! - SIMILARITY: BELONGS TO THE GALAPTIN (S-LECTIN) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q96DT0-4; Sequence=VSP_003100, VSP_003102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS A; B; C AND D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .me=B; Synonyms=GRIPla;
IsoId-Q96DT0-2; Sequence-VSP_003100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q96DT0-3; Sequence=VSP_003102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .me=E; Synonyms=1;
IsoId=Q96DT0-5; Sequence=VSP_003099;
.me=F; Synonyms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS B; E AND F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q96DT0-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21423969; PubMed=11435439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF244974; AAK77328.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF244975; AAK77329.1;
AF244976; AAK77330.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF310687; AAG40864.1;
EMBL; AF222695; AAF34677.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF244977; AAK77331.1;
EMBL; AF310686; AAG40863.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Adipose tissue;
                                                                                                                                                                                                                                  LGALS12 OR GRIP1.
                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
```

```
ó
Gaps
                                                                                                       0;
                                                                                           Query Match
46.4%; Score 52; DB 1; Length 336;
Best Local Similarity 57.1%; Pred. No. 1.4;
Matches 8; Conservative 3; Mismatches 3; Indels
                                                                                                                δ
```

Search completed: September 3, 2003, 11:46:59 Job time: 11.25 secs

qq

```
RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ogtuquo bos taurus

Ogxav5 bos taurus

Ogos79 gallus gall

Og1452 oncorhynchu

O31452 oncorhynchu

O31452 oncorhynchu

O31452 oromys lud

O39145 mus musculu

O34175 sus scrofa

O84137 homo sapien

O90710 gallus gall

O3uey4 homo sapien

O9uey5 homo sapien

O9uey5 homo sapien

O9uey6 homo sapien

O9uey6 homo sapien

O9uey6 homo sapien

O9uey6 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            091ze7 rattus norv
                                                                      September 3, 2003, 11:40:18 ; Search time 44.5 Seconds (without alignments) 115.979 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                            830525
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                 830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                OM protein - protein search, using sw model
                                                                                                                         US-10-087-464-1
104
1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q912E7
Q902E7
Q90579.
Q90579.
Q914F2
Q914F2
Q9175
Q90770
Q90710
Q90654
Q99654
Q99654
Q99654
                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                sp_fung1:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_mhc:*
sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                           SPTREMBL_23:*
: sp_archea:*
: sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp_plant:*
sp_rodent:*
sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1232
1241
1241
160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0
                                                                                                                                                                                                                                                                                                                                                                                                               Title:
Perfect score:
Sequence:
                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                                                                                   Searched:
                                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
Ю
```

ALIGNMENTS

														1						
				; ;	attus.			a									Gaps			
				eostom	nae; R			xchang								849;	0;			
		G	õ	a; Eutel	ae; Muri			anion e	abases.						RC64;	Length	Indels			
	AA.	Created) Last sequence update) Last annotation undate)	n in	ertebrat	Sciurognathi; Muridae; Murinae; Rattus.			of band 3	7DDBJ dat						E4B200780CB07D3A CRC64;	Score 104; DB 11;	, oe oe;			
	849 AA.) quence		ata; 1	ognath	-		tion c	; nBank/	•				; 1.	, 1. 007800	104;	matche			
	PRT;	Created Last sed		Crani			. W.M.;	teriza	colon." EMBL/Ge		change	1.		NGER_1	ANGER_2 E4B2		~``	20	1 677	
	INARY;	Lrel. 19, C	nge proteir	(rat). ; Chordata;	; Rodentia;		, Rajendrar	and charac	from rat c	K38733.1; -	7; Anion_ex 0: HCO3 cot	3_cotransp;	CO3TRNSPORT	PS00219; ANION_EXCHANGER_1;	ANION_EXCHANG 94312 MW;	100.08;	rative	GMPWLSATTVRSVTHANALT	GMPWI.SATTTVRSVTHANALT	· · · · · · · · · · · · · · · · · · ·
	PRELIMINARY;	(TrEMBLrel. (TrEMBLrel.	exchai	egicus Metazoa	utheria 10116;	OM N.A.	er H.J.	cloning	L) MRNA APR-200	382; AA	PR00171	55; HCO	1231; HGROOR3,	00219;	00220; 1 849 AA;	n cimilaritu	Conservative	WLSATT	TTT SATT	1
11.1	Q91ZE7 Q91ZE7:	01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2003 (TREMBLrel 23,	Battle norwegine (Pat)	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;	Mammalia; Eutheria; NCBI_TaxID=10116;	SEQUENCE FROM N.A.	Ye H., Binder H.J., Rajendran V.M.;	"Molecular cloning and characterization of band 3 anion exchange	protein (AEI) mRNA from rat colon."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases	EMBL; AY030082; AAK38733.1;	InterPro; IPR001717; Anion_exchange. InterPro: IPR003020: HCO3_cotranspt.	Pfam; PF00955; HCO3_cotransp;	PRINTS; PR01231; HCO3TRNSPORT.	PROSITE; PSC	PROSITE; PSC SEQUENCE 8	Query Match	Matches 20;	1 GMF	 - 	;
RESULT	ID O	ដ្ឋ	OE	88	000	RP 7	R A	RT	RI.	DR	DR DR	DR	DR DR	Z Z	SO	On	W	٥y	d	1

ó

RESULT 2

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                   090579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8JFT9
                                                                                                                                                                    RESULT 4
Q90579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
                                                                                     ò
                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                             TISSUE-Kidney;

Koshino I., Inaba M., Matsumoto M., Ono K.;

Koshino I., Inaba M., Matsumoto M., Ono K.;

Band 3 Bov. Nippon: a nonsense mutation in the band 3 gene associated with decreased mutant mRNA possessing dominant negative effect and dominant hereditary spherocytosis in cattle.";

Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

EMBL: AF163028; AAD43354-1;

HISSP; P02730; 1BNX.

InterPro; IPR001717; Anion_exchange.

InterPro; IPR003020; HC03_cotranspt.

Pfam; PP00955; HC03_cotranspt.

PRINTS; PR01231; HC03TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Bone marrow.

Koshino I., Inaba M., Matsumoto M., Ono K.;

Koshino I., Inaba M., Matsumoto M., Ono K.;

Koshino I., Inaba M., Matsumoto M., Ono K.;

Band 3 Bov. Nippon: a nonsense mutation in the band 3 gene associated with decreased mutant mRNA possessing dominant negative effect and dominant hereditary spherocytosis in cattle.";

Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AFIG 3826; AAAJ 393.1;

INTERPRO; IPRO01717; Anion_exchange.

InterPro; IPRO03120; HO3_cotranspt.

PRINTS; PRO1331; HC03_rotranspt.

PRINTS; PRO1331; HC03_TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                               Bos taurus (Bovine).
Bukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.1%; Score 101; DB 6; Length 85
95.0%; Pred. No. 1.1e-07;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGRFAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SEQUENCE 930 AA; 104374 MW; 4F6AADFEBAF6A3A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRULZJI, TORDOB34; ae; 1.
TICRFAMS; TICR06834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Band 3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                 855 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           930 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         663 GMPWLSATTVRTVTHANALT 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2003 (TrEMBLrel. 23, Band 3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 95.0
                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9913
               QUTUQ0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09XSW5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
Q9XSW5
Q9TUQ0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
Erythroid anion transporter.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cox J.V., Lazarides E.; "Alternative primary structures in the transmembrane domain of the chicken erythroid anion transporter."; Mol. Cell. Biol. 8:1327-1335(1988).
EMBL; M19496; AAA48604.1; --
HSSP; P02730; 1BTQ.
                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96.2%; Score 100; DB 13; Length 844; 90.0%; Pred. No. 1.6e-07; 1.ve 2; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 812;
                    Length 930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kimberley A.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL604064; CAD43432.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2002 (TrEMBLrel. 22, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
SI:0218065.1 (novel solute carrier protein) (Fragment).
SI:0218065.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001717; Anion_exchange.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR001201; HCO3_cotranspt.
FIGNS; PR001231; HCO3TRNSPORT.
IGRFAMS; TIGR00834; ae; 1.
PROSTITE; PS00219; ANION_EXCHANGER_1; 1.
SEQUENCE 844 AA; 93808 MW; C463F993D5974276 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   812 AA; 91488 MW; 855A5600C91E3073 CRC64;
Score 101; DB 6; Lv
Pred. No. 1.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 13;
                                                                                                                                                                                                                                                                                       844 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               812 AA
                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91.3%; Score 95;
                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                             653 GMPWLSATIVRIITHANALT 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=88216609; PubMed=2835670;
                                                                                                                 1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GMPWLSATTVRSVTHANALT 20
                    97.18;
95.08;
                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                    Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7955,
```

ö

Gaps

; 0

RESULT (

ò a

```
TISSUE-Stomach;
MEDLINE=9639307; PubMed=8756692;
Solotarey A.S., Chernova M.N., Yannoukakos D., Alper S.L.;
"Proteolytic cleavage sites of native AE2 anion exchanger in gastric
                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Straubberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002234; AAH02224.1;
R MGD; MGI:109351; S1C4a2.
R InterPro; IPR001717; Anion_exchange.
R InterPro; IPR001717; Anion_exchange.
R InterPro; IPR003020; HC03_cotranspt.
R Pfam; PF00555; HC03_cotranspt.
R PRINTS; PR01231; HC03_TRNSPORT.
DR TIGREAMS; TIGR00334; ae; 1.
                                                                               Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
   1 1 1 1 1 1 103 A 103 103 A 11012 MW; 29A99247E768B455 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER 1 1 SEQUENCE 466 AA; 52003 MW; 481C1108E28D03B1 CRC64;
                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 52.0 kDa protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09TU75;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Chloride-bicarbonate anion exchanger AE2 (Fragment)
                                                                             Score 93; DB 11; L4
Pred. No. 2.4e-07;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.4%; Score 93; DB 11;
85.0%; Pred. No. 1.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   622 AA.
                                                                                                                                                                                                                                                                                             466 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mucosal membranes.";
Biochemistry 35:10367-10376(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                         1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                               Query Match 89.4%;
Best Local Similarity 85.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
   NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                         Q99LT5
Q99LT5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9TU75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
Q9TU75
                                                                                                                                                                                                                                                       RESULT 8
                                                                                                                                                                                                                                                                           099115
     FT
                                                                                                                                                           Qγ
                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96080151; PubMed=7489705; Fievet B., Gabillat N., Borgese F., Motais R.; "Expression of band 3 anion exchanger induces chloride current and tearine transport: structure-function analysis."; EMBO J. 14:5158-5168(1995). EMBL; Z50848; CAA90701.1; -. HSSP; P02730; IBTO.
                                                                                                                                                                                                                                                                                       Anion exchanger.
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID=8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cynomys ludovicianus (Black-tailed prairie dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Gall bladder;
Abedin Z.R., Moser A.J., Roslyn J.J., Abedin M.Z.;
"Expression of anion exchange protein 2 (AE-2) in gallbladder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 95; DB 13; Length 912;
Pred. No. 1.1e-06;
1; Mismatches 1; Indels
                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       epithelia.";
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF012095; AAB66033.1;
InterPro; IFR0032020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotransp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; FROLSONS, 2007 1.
TIGRFAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         035225;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-2003 (TrEMBLrel. 23, Last annotation update)
L Similarity 90.0%; Pred. No. 9.8e-07; 18; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 AA
                                                                                                                                                                                               912 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfan; PF00955; HCO3_cotransp; 1.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anion exchange protein 2 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.3%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 90.0
nes 18; Conservative
                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=45480;
                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                             091452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         035225
```

Matches

ð 셤

RESULT 7

035225

ö

Gaps

.; 0

```
[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20090621;
                                      NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                     SLC4A2.
                                                                                                                                                                                                                                                                                                                                                          Q9UEY4
                                                                                                                                                                                                                                                                                                                                        RESULT 12
                                                                                                                                                                                                                                                                                                                                                29UEY
                                                                                                                                                                                                                                                                                                                                                                     δλ
                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                 Gaps
                           Zolotarev A.S., Shmukler B.E., Alper S.L.;
"AEZ anion exchanger polypeptide is a homooligomer in pig gastric membranes: a chemical cross-linking study.";
Biochemistry 38:8521-8531(1999).
EMBL; AF120099; AAF00977.1; -.
HSSP; P02730; 1BTQ.
                                                                                                                                                                                                                                                                                                                   01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUNAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
21 milar to solute carrier family 4, anion exchanger, member 2
(Erythrocyte membrane protein band 3-like 1).
Homo sapiens (Human).
Homo sapiens (Human).
Manmalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
WCBL_TaxID-9606;
                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89.4%; Score 93; DB 4; Length 1159;
85.0%; Pred. No. 3e-06;
tive 2; Mismatches 1; Indels
                                                                                                                                                                                        Score 93; DB 6; Length 622;
Pred. No. 1.6e-06;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO28601: AAH28601.1; -.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotransp; 1.
TGRFAMS; TIGR0084; ae; 1.
PROSITE: PS001219; ANION_EXCHANGER_1; 1.
PROSITE: PS001219; ANION_EXCHANGER_2; 1.
SEQUENCE 1159 AA; 127747 MW; 9F083A2BE8FF5D74 CRC64;
                                                                                                                                                              NON_TER 1 1
SEQUENCE 622 AA; 68713 MW; 58B013462C36E1DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                         1159 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1219 AA.
                                                                                      InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HC03_cotranspt.
PRINTS; PR01231; HC03TCNSPORT.
TIGRPAMS; TIGR00834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                        PRT;
                   MEDLINE-99315230; PubMed-10387099;
                                                                                                                                                                                                                                              1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                            89.4%;
85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 01, CTEMBLrel. 01, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 85.0%;
nes 17; Conservative
                                                                                                                                                                                      Query Match
Best Local Similarity 85.0°
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AE2-1 anion exchanger.
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (
01-NOV-1996 (
01-MAR-2003 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           090710
                                                                                                                                                                                                                                                                                                         Q8TAG3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                     RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEPTER B
g
```

```
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                            TISSUE=Proventriculus;
MEDLINE=96214107; PubMed-8621532;
COX K.H., Adair-Kir T.L., COX J.V.;
"Variant AE2 anion exchanger transcripts accumulate in multiple cell types in the chicken gastric epithelium.";
J. Balol. Chem. 271:8895-8902(1996).
EMBL; U48889; AR559881.1; -.
HSSP; P02730; 1BTQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Medina J.F., Lecanda J., Acin A., Ciesielczyk P., Prieto J.;
"Tissue-specific N-terminal isoforms from overlapping alternate promoters of the human AF2 anion exchanger gene.";
Biochem. Biophys. Res. Commun. 267:228-235(2000).
EMBL; U76669; AAF19584.2;
EMBL; U76669; AAF19584.2;
HSSP; P02730; IBTO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97179202; PubMed=9027488; Medina J.F., Acin A., Prieto J.; Medina J.F., Acin A., Prieto J.; Medina J.F., Acin and characterization of the human AE2 anion exchanger (SLC4A2) gene."; Genomics 39:74-85(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00955; HC03_cotransp; 1.
PRINTS; PR01231; HC03TRNSPORT.
TIGRRAMS; TIGRO0834; ae; 1.
PROSITE; PS00129; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SEQUENCE 1227 AA; 135577 MW; 5D47714C17FB8EF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00955; HCO3_cotransp; 1.
PRINTS; PR01231; HCO3TRNSPORT.
TIGRPAMS; TIGR00834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SEQUENCE 1219 AA; 135288 WW; 25F42A73C3483B21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2003 (TrEMBLrel. 23, Last annotation update)
Anion exchanger 2 type b1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.4%; Score 93; DB 13;
85.0%; Pred. No. 3.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1227 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
```

; 0 ö

Gaps

;

Score 93; DB 4; Length 1241; Pred. No. 3.2e-06; 2; Mismatches 1; Indels

89.4%; 85.0%;

```
Medina J.F., Acin A., Prieto J.;
"Molecular cloning and characterization of the human AE2 anion exchanger (SLC4A2) gene.";
Genomics 39:74-85(1997).
BMB.; U62531; AAC50964.1; -.
                                                                                              InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotranspt.
PR01231; HCO3_TRNSPORT.
IIGRFAMS; TIGR00834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SEQUENCE 1241 AA; 137009 MW; D266ECDAB238FD97 CRC64;
                                                                                                                                                                                                                                                                            1050 GLPWLAAATVRSVTHANALT 1069
              MEDLINE=97179202; PubMed=9027488;
                                                                                                                                                                                                                                                               1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                             Query Match
Best Local Similarity 85.0°
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20090621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                               O9UEY6;
                                                                                                                                                                                                                                                                                                                                                  Q9UEY6
                                                                                                                                                                                                                                                                                                                                                                                                                             SLC4A2
                                                                                                                                                                                                                                                                                                                          RESULT 15
                                                                                                                                                                                                                                                                                                                                       Q9UEY6
                qq
                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                      ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        Medina J.F., Lecanda J., Acin A., Ciesielczyk P., Prieto J.;

"Tissue-specific N-terminal isoforms from overlapping alternate promoters of the human AE2 anion exchanger gene.";

Blochem. Biophys. Res. Commun. 267:228-235(2000).

REMBL; U76669; AAF23240.1; --

REMBL; U76669; AAF23240.1; JOINED.

REMBL; U76668; AAF23240.1; JOINED.

REMBL; U76609; AG0220; HG03_cotranspt.

REMBL; PRO0955; HG03_cotranspt.

R Pfam; PF00955; HG03_cotranspt.

R TIGRAMS; TIGROWS 41; ae; 1.

R PROSITE; PS00210; ANION_EXCHANGER_1; 1.

R PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                     ;
0
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=97179202; PubMed=9027488;
Medina J.F., Acin A., Prieto J.;
Molecular cloning and characterization of the human AE2 anion exchanger (SLC4A2) gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.4%; Score 93; DB 4; Length 1232; 85.0%; Pred. No. 3.2e-06; ive 2; Mismatches 1; Indels
              Length 1227;
                                     1; Indels
                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
           Score 93; DB 4; 1 Pred. No. 3.2e-06;
                                                                                                                                                  1232 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1241 AA
                                     2; Mismatches
                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                  PRT;
                                                                          1041 GLPWLAAATVRSVTHANALT 1060
                                                             1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GMPWLSATTVRSVTHANALT 20
           89.4%;
85.0%;
                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2003 (TrEMBLrel. 23, Anion exchanger 2 type b2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1997 (TrEMBLrel. 03, 01-MAY-1997 (TrEMBLrel. 03, 01-MAR-2003 (TrEMBLrel. 23, AEZ anion exchanger.
Query Match
Best Local Similarity 85.v.
The conservative 17; Conservative 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 85.0 ses 17; Conservative
                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20090621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q99654
Q99654;
                                                                                                                                                Q9UEYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLC4A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
099654
                                                                                                                        RESULT 13
                                                                                                                                      Q9UEY5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                     셤
                                                                                                                                                  å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Medina J.F., Lecanda J., Acin A., Ciesielczyk P., Prieto J.;
"Tissue-specific N-terminal isoforms from overlapping alternate promoters of the human AE2 anion exchanger gene.";
Biochem. Biophys. Res. Commun. 267:228-235(2000).
EMBL; U76669; AAF19583.2; -...
EMBL; U76669; AAF19583.2; JOINED.
EMBL; U76668; AAF19583.2; JOINED.
HSSP; P02730; 1BTQ.
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=97179202; PubMed=9027488;
Medina J.F., Acin A., Prieto J.;
"Molecular cloning and characterization of the human AE2 anion exchanger (SLC4A2) gene.";
Genomics 39:74-85(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 89.4%; Score 93; DB 4; Length 1241; Best Local Similarity 85.0%; Pred. No. 3.2e-06; Matches 17; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGRAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE: PS00220; ANION_EXCHANGER_2; 1.
SEQUENCE 1241 AA; 136980 MW; D2FDA72E20D70D64 CRC64;
                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotranspt.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                            Anion exchanger 2 type a.
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
```

Search completed: September 3, 2003, 11:50:01 Job time : 46.5 secs

```
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

US-10-087-464-1 104 Title: Perfect score:

1 GMPWLSATTVRSVTHANALT 20 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

830525 Total number of hits satisfying chosen parameters:

830525 seqs, 258052604 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match,100% Listing first 45 'summaries

sp_archea:*
sp_bacteria:*
sp_fung:*
sp_human:*
sp_nvertebrate:*
sp_mammal:* sp_virus:*
sp_vertebrate:*
sp_unclassified:* sp_rvirus:*
sp_bacteriap:*
sp_archeap:* sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:* SPTREMBL_23:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	091ze7 rattus norv	O9tug0 bos taurus	09xsw5 bos taurus	090579 gallus gall	081ft9 brachydanio	091452 oncorhynchu	035225 cynomys lud	0991t5 mus musculu	09tu75 sus scrofa	O8tag3 homo sapien	090710 qallus qall	Oguev4 homo sapien	Oguev5 homo sapten	099654 homo sapten	Oguevé homo sapien	P79877 lampetra ja
1	ΩI	1 Q91ZE7	O9TUQ0	O9XSW5	3 090579.	3 QBJFT9	3 091452	1 035225	1 099LT5	Q9TU75	QBTAG3	3 Q90710	Q9UEY4	Q9UEY5	099654	Q9UEY6	3 P79877
	Query Match Length DB			930 6	844 13	812 13	912 13	103 11	466 11	622 6	1159 4	1219 13	1227 4	1232 4	1241 4	1241 4	160 13
di	Query	100.0	97.1	97.1	96.3	91.3	91.3	89.4	89.4	89.4	89.4	89.4	89.4	89.4	89.4	89.4	85.6
	Score	104	101	101	100	95	95	93	93	93	93	93	93	93	93	93	83
	Result No.	-	7	٣	4	2	9		œ	ტ	10	11	12	13	14	. 15	16

Ogerp4 mus musculu Ogerp5 mus musculu Ogudjl homo sapien Og9416 homo sapien O13717 homo sapien	droso droso droso droso	USYC48 uC9SOPNIIA 095233 homo sapien 08cfs3 mus musculu Q9neg6 homo sapien 09est0 mus musculu	3 mus 6 mus 6 mus 7 mus 7 mus	Q8bwz4 mus musculu Q9uib9 homo sapien O60350 homo sapien Q9hc88 homo sapien Q9y6m7 homo sapien Q9yfm7 arttus norv	Q9qyd5 rattus norv Q9r111 rattus norv Q9vm32 drosophila
Q9ERP4 Q9ERP5 Q9UDJ1 Q99416 Q13717	0955W2 08MRK3 081QD4 081QD6 081QD6	095233 095233 09CFS3 09HCQ6 09EST0	Q8C943 Q9JKV6 Q8JZR6 Q8BY17 O94843	Q8BWZ4 Q9UIB9 O60350 Q9HC88 Q9Y6M7 Q9R1N3	090YD5 09R1L1 09VM32
111444	របសសសស	11 4 11 11 11 11 11 11 11 11 11 11 11 11	111114	11 4 4 4 4 11 11	11 11 5
1030 1227 124 357 357	.467 914 1161 1201 1228	1044 1087 1088 1088	1088 1089 1089 1089	651 1000 1018 1090 1214 1218	1241 1254 1030
85.6 85.6 80.8 80.8	000000	603334 633.576 633.576	m m m m m	0000000 000000 000000	59.6 59.6 58.7
88 89 8.5 84 84	22222	9999	00000		62 62 61
17 18 19 20 21	22222 2222 2224 32	28 30 31		C E E E E E E E E E E E E E E E E E E E	4 4 4 6 4 4 5 4 5

ALIGNMENTS

stomi; 2; Rattus.	<u>.</u>	0; Gaps
i naci	849	
te) ta; Eute dae; Mur 3 anion	ERC64; Length 849;	Indels
AA. update on upda ertebra ii; Murii	ranspt. 1. NGER_1; 1. NGER_2; 1. E4B200780CB07D3A CRC64; Score 104; DB 11; Leng Pred. No. 3.6e-08;	: n
849 AA. uence up otation tta; Vert gnathi; ion of b	1. 10.7800 104;	atche
PRT; reated) ast seq ast seq ast ann Crania Sciurc Sciurc V.M.; terizat terizat terizat MBL/Gen	ranspt. 1. NGER_1; NGER_2; E4B20 Score Pred.	0; Mismatches
17. 1 9012E7 PRELIMINARY; PRT; 849 AA. 9012E7, Created) 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2003 (TrEMBLrel. 23, Last annotation update) Band 3 anion exchange protein. Battus norvegicus (Rat). Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Battus norvegicus (Rat). Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Battus norvegicus (Rat). Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi; NCBI_TaxID=10116; [1] NCBI_TaxID=10116; [1] Familia in	Interpro; IPR003020; HC03_cotranspt. Pfam; PF00955; HC03_cotransp; 1. PRINIES, PR01231; HC03TRNSPORT. TIGREAMS; TIGR00834; ae; 1. PROSITE; PS00219; ANION_EXCHANGER_1; 1 PROSITE; PS00220; ANION_EXCHANGER_2; 1 SEQUENCE 849 AA; 94312 MW; E4B2007; IY Match 100.0%; Score 10. IL Local Similarity 100.0%; Pred No	
T 1 7 0912E7 9012E7 01-DEC-2001 (TrEMBLrel. 01-MAR-2003 (TrEMBLrel. 01-MAR-2001 (TremBLrel.) 01-MA	InterPro; IPR003020; HC03_C Pfam; PF00955; HC03_cotrans PRINTS; PR01231; HC03TRNSPO TICRFAMS; TICR00844; ae; 11. PROSITE; PS00219; ANION_EXC PROSITE; PS00220; ANION_EXC SEQUENCE 849 AA; 94312 M IY Match 100.08	20; Conservative
7 1 7 1 7 1 7 1 7 1 7 1 7 1 7 1 7 1 7 1	InterPro; IPR003020 Pfam; PF00955; HC0 PRINTS; PR01231; HC0 TIGREAMS; TIGRE0083; PROSITE; PS00219; PS00217E; PS00220; ESQUENCE 849 AA; Query Match	
RESULT 1 0912E7 AC 0912E7 O912E7 DT 01-DEC DT 01-DEC DT 01-MAR DE Band 3 OC ENARY OC MAMMAIN OC NCBL_T RR (1) RR (InterPro Pfan; PF PRINTS; TICRRAMS; PROSITE; PROSITE; SEQUENCE Query Match	Matches
PESON ON CONTRACT OF THE PROPERTY OF THE PROPE	SO S	≥;

RESULT 2

g δ

ó

THIS PAGE BLANK (USPTO)

```
NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                            738
                                                                                                                                                                                                                         090579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QBJFT9;
                                                                                                                                                                                                                                                                                                                                                                                                              Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OBJFT9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
                                                                                                                                                                                        RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8JFT9
                                                                                                                                                                                                         090579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC AC DIT DIT SEE BY SE
                                                                                                                                                                                                                                                Óγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                         à
                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Koshino I., Thaba M., Matsumoto M., Ono K.;
Koshino I., Thaba M., Matsumoto M., Ono K.;
"Band 3 Bov. Nippon: a nonsense mutation in the band 3 gene associated
with decreased mutant mRNA possessing dominant negative effect and
dominant hereditary spherocytosis in cattle.";
submitted (JUV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF1688128; AAD43354.1; -.
HSSP; PO2730; IBNX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                            Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.1%; Score 101; DB 6; Length 85
95.0%; Pred. No. 1.1e-07;
Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINES, FROLES, ...
TIGREAMS; TIGEO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGREAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SEQUENCE 855 AA; 95643 MW; 06CD037324F69872 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ą
              855 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TIEMBLEEL. 12, Created)
01-NOV-1999 (TIEMBLEEL. 12, Last seq
01-MAR-2003 (TIEMBLEEL. 23, Last anno
Band 3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR001717; Anion_exchange.
Interpro; IPR0030050; HGO3_cotranspt.
Pfam. Pf00955; HCO3_cotranspt. 1.
PRINYS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR001717; Anion_exchange.
Interpro; IPR003020; HC03_cctranspt.
Pfam, PF00955; HC03_cctranspt.
PRINTS; PR01231; HC03TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GMPWLSATTVRSVTHANALT 20
                                                     01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 97.1
Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9913;
                                                                                                                  Band 3 protein.
                                                                                                                                                                                                                                                                                              TISSUE-Kidney
                                     Q9TUQ0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O9XSW5
                  09TU00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BEB3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
Q9XSW5
09TU00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQ
```

```
ö
                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                       PERFORMED FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-88216609; PubMed-2835670;

A Cox J.V., Lazaratides E.;

"Alternative primary structures in the transmembrane domain of the chicken erythroid anion transporter.";

MOI. Cell. Biol. 8.1327-1335(1988).

EMBL. M19496; AAA48604.1; -.

R ESSP: P02730; 1BTO.

InterPro; IPR001717; Anion_exchange.

InterPro; IPR00320; HCO3_cotranspt.

PRINTS; PR01231; HCO3TRNSPORT.

TIGROWS 1 HCO3TRNSPORT.

TIGROWS 21; HCO3TRNSPORT.

PRINTS; PS00220; ANION_EXCHANGER_1; 1.

PROSITE; PS00220; ANION_EXCHANGER_2; 1.

PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                          Erythroid anion transporter.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 812;
Score 101; DB 6; Length 930;
Pred. No. 1.2e-07;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kimberley A.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: AL604064; CAD44432.2; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91488 MW; 855A5600C91E3073 CRC64;
                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 100; DB 13;
Pred. No. 1.6e-07;
3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                812 AA.
                                                                                                                                                                                                        844 AA.
                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.3%; Score 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        653 GMPWLSATTVRTITHANALT 672
                                                                                                1 GMPWLSATTVRSVTHANALT 20
                                                                           1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.2%;
90.0%;
   97.1%;
95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 90.09
   Query Match 97.1
Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         812 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
```

THIS PAGE BLANK (USPTO)